

92655

STIC-Biotech/ChemLib

From: Mehta, Ashwin
Sent: Monday, April 28, 2003 4:11 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

STIC,

Please search the commercial and interference databases for the following from 09/845,849:

- 1) the nucleotide sequence of SEQ ID NO: 1
- 2) the nucleotide sequence of SEQ ID NO: 3

My mail room is 9E12, office 9E07, art unit 1638.

Thank you,
Ashwin

Ashwin Mehta
United States Patent and Trademark Office
Biotechnology Patent Examiner
703-306-4540

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/29
Date Completed: 5/5
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 15:58:02 ; Search time 2798 Seconds

(without alignments)
8903.503 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856
Sequence: 1 tctgaactatgtagtcccc.....aaaaaaaaaaaactcgag 856Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pin:*
35: em_hgt_rtd:*
36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgtgo_hum:*
40: em_hgtgo_mus:*
41: em_hgtgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	856	100.0	856	6	ARI48907	ARI48907 Sequence
2	842.4	98.4	855	6	ARI48906	ARI48906 Sequence
3	799.6	93.4	864	8	AB027504	AB027504 Arabidops
4	763.4	89.2	840	8	AY065378	AY065378 Arabidops
5	635.6	74.3	780	8	AB027505	AB027505 Arabidops
6	559	65.3	559	8	AY133813	AY133813 Arabidops
7	528	61.7	528	6	E38985	E38985 Method for
8	466	54.4	109560	8	F5114	AC001229 Sequence
9	465	54.3	2483	8	AF152096	AF152096 Arabidops
10	389.8	45.5	799	8	AB027506	AB027506 Arabidops
11	377.6	44.1	528	8	AF152907	AF152907 Arabidops
12	374.4	43.7	528	6	E38986	E38986 Method for
13	289.6	33.8	745	8	AB027456	AB027456 Citrus un
14	248.8	29.1	899	6	AX478001	AX478001 Sequence
15	248.4	29.0	847	8	AB052943	AB052943 Oryza sat
16	248	29.0	847	8	AB052944	AB052944 Oryza sat
17	239.8	28.0	1004	6	AX478049	AX478049 Sequence
18	238.6	27.9	866	8	AB062676	AB062676 Oryza sat
19	230.4	26.9	1191	6	AX478007	AX478007 Sequence
20	225.2	26.3	1078	6	AX477997	AX477997 Sequence
21	220.6	25.8	886	6	AX478033	AX478033 Sequence
22	196	22.9	836	6	AX478029	AX478029 Sequence
23	187	21.8	969	6	AX478027	AX478027 Sequence
24	185.8	21.7	492	6	AX477991	AX477991 Sequence
25	176.8	20.7	668	6	A61530	A61530 Sequence 4
26	176.8	20.7	668	8	ATU77674	U77674 Arabidops
27	175	20.4	837	6	AX478005	AX478005 Sequence
28	174.4	20.4	954	8	AF316419	AF316419 Lolium pe
29	171.6	20.0	950	8	AF159882	AF159882 Oryza sat
30	168.8	19.7	597	8	AB024715	AB024715 Arabidops
31	168.8	19.7	886	8	AY065211	AY065211 Arabidops
32	168.4	19.7	613	6	AX478043	AX478043 Sequence
33	166.8	19.5	559	8	AY096515	AY096515 Arabidops
34	166.4	19.4	980	6	AX478011	AX478011 Sequence
C 35	164	19.2	109936	8	ATCFE13	AL080253 Arabidops
36	164	19.2	197568	8	ATCFE13	AL15553 Arabidops
37	160.6	18.8	577	8	AF145259	AF145259 Nicotiana
38	159.4	18.6	902	6	AX478009	AX478009 Sequence
39	159	18.6	907	8	AF159883	AF159883 Oryza sat
40	157.6	18.4	1295	6	AX478021	AX478021 Sequence
41	154.8	18.1	560	8	AF145260	AF145260 Nicotiana
42	154.4	18.0	869	8	LEU84140	U84140 Lycopersico
43	146.8	17.1	558	8	AF145261	AF145261 Nicotiana
44	145.8	17.0	4377	8	ATU67834	U67834 Arabidops
45	136	15.9	354	8	AF145262	AF145262 Nicotiana

ALIGNMENTS

RESULT 1
ARI48907/c
LOCUS ARI48907 856 bp DNA
DEFINITION Sequence 3 from patent US 6225530.
ACCESSION ARI48907
VERSION ARI48907.1 GI:15112997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 856)
AUTHORS Weigel, D. and Kaul, A. I.
TITLE Flowering locus T (FT) and genetically modified plants having modulated flower development
JOURNAL Patent: US 6225530-A 3 01-MAY-2001

FEATURES
Source Location/Qualifiers
1.856
/organism="unknown"
BASE COUNT 249 a 194 c 150 g 263 t
ORIGIN

Query Match 100.0%; Score 856; DB 6; Length 856;
Best Local Similarity 100.0%; Pred. No. 7.1e-192;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
DB 856 TCTAGAACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 797
QY 61 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGTTGAGAGCTTCTTG 120
DB 796 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGTTGAGAGCTTCTTG 737
QY 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCCCCAAGAGAGTGAATAG 180
DB 736 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCCCCAAGAGAGTGAATAG 677
QY 181 GCTTGATCTAAGGCTCTGAGTTCAAAACAGCCAAAGAGTTGATGTTGGTGAAG 240
DB 676 GCTTGATCTAAGGCTCTGAGTTCAAAACAGCCAAAGAGTTGATGTTGGTGAAG 617
QY 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCGATGCTCAAGTCCCTAGCAAC 300
DB 616 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCGATGCTCAAGTCCCTAGCAAC 557
QY 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
DB 556 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 497
QY 361 CCTTGGCAATGAGATTTGTGTTGACAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
DB 496 CCTTGGCAATGAGATTTGTGTTGACAAATCCAAAGTCCCACTCAGAGAAATTCATG 437
QY 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
DB 436 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 377
QY 481 AGAAGCTCAACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCCGTGGCCGAG 540
DB 376 AGAAGCTCAACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCCGTGGCCGAG 317
QY 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
DB 316 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 257
QY 601 CCTTATTAACCAATGATATGATCTGATGATGATGATGATGATGATGATGATGATG 660
DB 256 CCTTATTAACCAATGATATGATCTGATGATGATGATGATGATGATGATGATGATG 197
QY 661 TTTTATTAACCAATTTATGATACGATACGAACGCTGATGATGATGATGATGATGATG 720
DB 196 TTTTATTAACCAATTTATGATACGATACGAACGCTGATGATGATGATGATGATGATG 137
QY 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780
DB 136 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 77
QY 781 TGTGATGCGATTAATTAATTAATCTACATGAATGAAGTGTATTAATTAATTAATTA 840
DB 76 TGTGATGCGATTAATTAATTAATCTACATGAATGAAGTGTATTAATTAATTAATTA 17
QY 841 AAAAAAAAAAAGTCTGAG 856
DB 16 AAAAAAAAAAAGTCTGAG 1

LOCUS ARI48906 855 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 622530.
ACCESSION ARI48906
VERSION ARI48906.1 GI:15112996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 855)
AUTHORS Weigel, D. and Kardallsky, I.
TITLE Flowering locus T (FT) and genetically modified plants having
JOURNAL modulated flower development
PATENT Patent: US 622530-A 1 01-May-2001;
FEATURES location/Qualifiers
source 1.855
BASE COUNT 263 a 151 c 193 g 248 t
ORIGIN

Query Match 98.4%; Score 842.4; DB 6; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-188;
Matches 854; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 TCTAGACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
DB 1 TCTAGAACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
QY 61 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGTTGAGAGCTTCTTG 120
DB 61 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGTTGAGAGCTTCTTG 120
QY 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCCCCAAGAGAGTGAATAG 180
DB 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCCCCAAGAGAGTGAATAG 180
QY 181 GCTTGATCTAAGGCTCTGAGTTCAAAACAGCCAAAGAGTTGATGTTGGTGAAG 240
DB 181 GCTTGATCTAAGGCTCTGAGTTCAAAACAGCCAAAGAGTTGATGTTGGTGAAG 240
QY 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATGATGATGATGATGATGATGATG 300
DB 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATGATGATGATGATGATGATGATG 300
QY 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
DB 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
QY 361 CCTTGGCAATGAGATTTGTGTTGACAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
DB 361 CCTTGGCAATGAGATTTGTGTTGACAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
QY 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
DB 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
QY 481 AGAAGCTCAACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCCGTGGCCGAG 540
DB 481 AGAAGCTCAACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCCGTGGCCGAG 540
QY 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
DB 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
QY 601 CCTTATTAACCAATGATATGATCTGATGATGATGATGATGATGATGATGATGATG 660
DB 601 CCTTATTAACCAATGATATGATCTGATGATGATGATGATGATGATGATGATGATG 660
QY 661 TTTTATTAACCAATTTATGATACGATACGAACGCTGATGATGATGATGATGATGATG 720
DB 660 TTTTATTAACCAATTTATGATACGATACGAACGCTGATGATGATGATGATGATGATG 719
QY 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780
DB 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780

QY	45	GTTTGTCACAAATCAAAAGATGCTATATAATTAAGAGACCCCTTTATGTGAAGAGACTT	104
Db	52	GTTTGTCACAAATCAAAAGATGCTATATAATTAAGAGACCCCTTTATGTGAAGAGACTT	111
QY	105	GTTCGAGACGTTCTTGATCCGTTTAATATGATCAATCACTCTPAAGTTACTTATGGCCAA	164
Db	112	GTTCGAGACGTTCTTGATCCGTTTAATATGATCAATCACTCTPAAGTTACTTATGGCCAA	171
QY	165	AGAGAGGAGATTAATGGCTTGGATCTAAGGCCCTCTCAGGTTCCAAACAACCAAGACTT	224
Db	172	AGAGAGGAGATTAATGGCTTGGATCTAAGGCCCTCTCAGGTTCCAAACAACCAAGACTT	231
QY	225	GAGATTTGGTGAAGAAGACCTCAGAACTCTATACCTTTGGTATGGTATGCAGATGTT	284
Db	232	GAGATTTGGTGAAGAAGACCTCAGAACTCTATACCTTTGGTATGGTATGCAGATGTT	291
QY	285	CCAAAGTCTAGCAACCTCACCCTCCGAGATATCTCCATGTTGGTGGTACTGATATCCCT	344
Db	292	CCAAAGTCTAGCAACCTCACCCTCCGAGATATCTCCATGTTGGTGGTACTGATATCCCT	351
QY	345	GCTCAACTGGAAACAACCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACT	404
Db	352	GCTCAACTGGAAACAACCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACT	411
QY	405	GCAGGAATTCATCGTGTGCTTTATATGTTTGCACAGCTGGCAGGCAAAAGTGTAT	464
Db	412	GCAGGAATTCATCGTGTGCTTTATATGTTTGCACAGCTGGCAGGCAAAAGTGTAT	471
QY	465	GCACCAGGAGGCGCCAGCACTTCAACACTGCGAGTTTGTGAGATCTACATCTCGGC	524
Db	472	GCACCAGGAGGCGCCAGCACTTCAACACTGCGAGTTTGTGAGATCTACATCTCGGC	531
QY	525	CTTCCCGTGGCGGAGTTTCTACAATGTGCAGAGGGAGAGTGGTGGGAGGAAGA	584
Db	532	CTTCCCGTGGCGGAGTTTCTACAATGTGCAGAGGGAGAGTGGTGGGAGGAAGA	591
QY	585	CTTTAGATGGCTTCTCTCTTTATAACCAATGATATTGTCATCTGTGATGATTTATGC	644
Db	592	CTTTAGATGGCTTCTCTCTTTATAACCAATGATATTGTCATCTGTGATGATTTATGC	651
QY	645	ATCTATAGTATTTTATTTAATTAACCAATTTTATGATACGAGTAAACGAACGGTATGATGC	704
Db	652	ATCTATAGTATTTTATTTAATTAACCAATTTTATGATACGAGTAAACGAACGGTATGATGC	711
QY	705	CTATAGTGTCCAAATATTAAGTGTGATATAAATGAGAGGGGAGGAAATGAGAGTG	764
Db	712	CTATAGTGTCCAAATATTAAGTGTGATATAAATGAGAGGGGAGGAAATGAGAGTG	771
QY	765	TTTTACTATATAGTGTGATGCATTAATATATTTAACTACATGAATGAAGTGTAT	824
Db	772	TTTTACTATATAGTGTGATGCATTAATATATTTAACTACATGAATGAAGTGTAT	831
QY	825	ATTATATAAAAAAAAAAAAAA 850	
Db	832	ATTATATAAAAAAAAAAAAAA 857	
RESULT 4			
LOCUS	AY065378	840 bp	mRNA
DEFINITION	Arabidopsis thaliana putative flowering signals mediating protein		
ACCESSION	AY065378		
VERSION	AY065378.1	GI:17529185	
KEYWORDS	FLI-CDNA.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 840)		
AUTHORS	Yamada, K., Liu, S.-X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,		

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carinici, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 840)

Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carinici, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

TITLE
JOURNAL
COMMENT

Direct Submission

Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carinici, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers

1. 840

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="1"

/clone="RAFL06-80-B19 (R11796)"

/note="This clone is in a modified pBluescript vector (Lambda ZAP) as a XhoI/SstI insert."

ecotype: Columbia"

1. 840

/gene="Atlg65480"

1. 82

/gene="Atlg65480"

83. 610

/gene="Atlg65480"

/codon_start=1

/evidence="experimental"

/product="putative flowering signals mediating protein FT"

/protein_id="AAL38819.1"

/db_xref="GI:17529186"

/translation="MSINIRDPILVSRVGVDPILPFNRSITLKYQGREVTNGIDLR

PSOVNKRVEIGEDLRFNFTLVAVDPSVPHLRETLMLVTQIDPATPTGTTGS

NEIYCEPSPFTAGIHRVFTLLFRLQSGQTYVAAQWQNGNFTREAEIYNGLPVAAV

FYNCRBSGCGGRLL"

611. 840

/gene="Atlg65480"

276 a 148 c 182 g 234 t

BASE COUNT

ORIGIN

Query Match 89.2% Score 763.4; DB 8; Length 840;

Best Local Similarity 99.2% Pred. No. 5.4e-170;

Matches 767; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

45 GTTGTCAAGATCAAGTGTCTAATAATATAAGACCCCTTATGTAGACAGATT 104

|||||

Db 65 GTTGTCAAGATCAAGATGTCTAATAATATAAGACCCCTTATGTAGACAGATT 124

Qy 105 GTTGTGAGCTTCTTGATCCGTTTAAATAGATCAATCACTCTAAAGTACTTATGGCCAA 164

Db 125 GTTGTGAGCTTCTTGATCCGTTTAAATAGATCAATCACTCTAAAGTACTTATGGCCAA 184

Qy 165 AGAGAGCTACTAATGCTTGGATCTAAGCCCTTCCAGTTCAAAACAGCAAGAGTT 224

Db 185 AGAGAGCTACTAATGCTTGGATCTAAGCCCTTCCAGTTCAAAACAGCAAGAGTT 244

Qy 225 GAGATTGGTGAGAGAGAGCTCAGAGAACTCTTACTTGGTATGTTGATGATCAATGTT 284

Db 245 GAGATTGGTGAGAGAGAGCTCAGAGAACTCTTACTTGGTATGTTGATGATCAATGTT 304

Qy 285 CCAAGTCCAGAGAGAGAGCTCAGAGAACTCTTACTTGGTATGTTGATGATCAATGTT 344

Db 305 CCAAGTCCAGAGAGAGAGCTCAGAGAACTCTTACTTGGTATGTTGATGATCAATGTT 364

Qy 345 GCTACAACTGGAACAACCTTTGGCAATGATGTTGTTACGAATAATCAAGTCCACT 404

Db 365 GCTACAACTGGAACAACCTTTGGCAATGATGTTGTTACGAATAATCAAGTCCACT 424

Qy 405 GCAGGAATTCATGCTGCTGCTTTATGTTTTCAGACAGCTTGGCAGGCAAGAGTAT 464

Db 425 GCAGGAATTCATGCTGCTGCTTTATGTTTTCAGACAGCTTGGCAGGCAAGAGTAT 484

Qy 465 GCACCAAGTGGCGCCAGAACTTCAACACTCGAGATTGCTGAGATCTACATCTCGGC 524

Db 485 GCACCAAGTGGCGCCAGAACTTCAACACTCGAGATTGCTGAGATCTACATCTCGGC 544

Qy 525 GTTCCCGTGGCGCGAGTTTTCACAACTTTCAGAGGAGAGTGGCTGGCAGGAAGA 584

Db 545 GTTCCCGTGGCGCGAGTTTTCACAACTTTCAGAGGAGAGTGGCTGGCAGGAAGA 604

Qy 585 GTTACAGTGGCTTCTTCTTATTAACCAATGATATGATCTGATGATGATTTATG 644

Db 605 GTTACAGTGGCTTCTTCTTATTAACCAATGATATGATCTGATGATGATTTATG 664

Qy 645 ATCTATAGTATTTTATTAATTAATTAACCAATTTTATGATGATGATGATGATG 704

Db 665 ATCTATAGTATTTTATTAATTAATTAATTAACCAATTTTATGATGATGATGATG 724

Qy 705 CATATGATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 764

Db 725 CATATGATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 784

Qy 765 TTTTACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 817

Db 785 TTTTACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837

RESULT 5 780 bp mRNA linear PLN 26-FEB-2000

AB027505 Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds,

LOCUS AB027505.1

DEFINITION Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds,

ACCESSION AB027505.1

VERSION AB027505.1

KEYWORDS FT.

SOURCE Arabidopsis thaliana (strain Landsberg er) cDNA to mRNA.

ORGANISM Arabidopsis thaliana

REFERENCE Arabidopsis thaliana (strain Landsberg er) cDNA to mRNA.

Arabidopsis thaliana (strain Landsberg er) cDNA to mRNA.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (sites)

Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.

A pair of related genes with antagonistic roles in mediating

flowering signals

Science 286 (5446), 1960-1962 (1999)

JOURNAL MEDLINE 20050958

REFERENCE 2 (bases 1 to 780)

Araiki, T. and Kobayashi, Y.

Direct Submission

JOURNAL Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science
Kyoto University, Department of Botany, Division of Biological
Sciences, Sakyo-ku, Kyoto 606-8502, Japan
(E-mail: taraku@gr.bot.kyoto-u.ac.jp, Tel: 81-75-753-4136,
Fax: 81-75-753-4141)

QY 543 TTCTACATTGTGAGAGGAGTGGCTGGAGAGAGACTTAG 590
|||||
Db 481 TTTCACATTGTGAGAGGAGAGTGGCTGGAGAGAGACTTAG 528
|||||

RESULT 8
F5114 109560 bp DNA linear PLN 11-JUN-1997
LOCUS Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1,
DEFINITION complete sequence.
AC001229
VERSION AC001229.1 GI:2182285
KEYWORDS HTG.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 109560)
Vysotskaya,V.S., Osborne,B.I., Toriumi,M., Yu,G., Oji,O.,
Shen,Y.K., Buehler,E., Conway,A.B., Conway,A.R., Dewar,K., Feng,J.,
Kim,C., Kurtz,D., Li,Y., Shinn,P., Sun,H., Davis,R.W., Ecker,J.R.,
Fedorov,N.A. and Theologis,A.
The sequence of BAC F5114 from Arabidopsis thaliana chromosome 1
Unpublished (1997)
2 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (15-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (17-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (06-JUN-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
5 (bases 1 to 109560)
Theologis,A.
Direct Submission
Submitted (11-JUN-1997)
On Jun 10, 1997 this sequence version replaced gi:1943864.
COMMENT
FEATURES
Source
Location/Qualifiers
1. 109560
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
complement(129..1191)
/gene="F5114.1"
complement(join(129..327,950..1191))
/gene="F5114.1"
/codon_start=1
/evidence=not_experimental
/protein_id="AA860919.1"
/db_xref="GI:2190535"
/translation="MRRQPKSELPKILKSTNSGVTSDEPNNKQDGCENNFDR
OCKSSNRKSRVKKLOLFQDKSCRPFGIMPSOTCLNTKDHVVIKILYRRK
LVKAFIVRMKTKVWKVDYORLMMKVIKMTLMCLMDSQKKR"
complement(1312..2949)
/gene="F5114.2"
complement(join(1312..1701,1833..1956,2039..2186,
2268..2367,2491..2949))
/gene="F5114.2"
/codon_start=1
/evidence=not_experimental
/protein_id="AA860903.1"
/db_xref="GI:2190539"
/translation="MDEVSTVNNENKRTMIEPKLNRKREPALINLTSEEKSOI
SINLEMKGLFDYFREVMDSKRTDLFSGSECSLSNSVALLMEMSLPLSKLVDEI
YLKTEKTESVMAVAVSVGQVSYGLNVADVAILEDSESLMCWETDLKIM
PSSRVGLKLRPRCKIHERITAVSMLALREERETKMRSDLSRAAKLKITSE
VDLRSPDMNMOKNSSSEMAKDSKREPKILLKOLEKRCARAEKREKROYLKEIKO
OEKBOUKLOKAIYDNNKEKEETESKRRIKKQDESEKEDKREKDAELKKLOLVOK
QASIMERFLKSKSDSLTPRLPSSEVTAOELCTKHENIGVAVQADNAVSTTCEA
TVDDIRRYDIGSPC"
complement(10580..12759)
/gene="F5114.3"
join(10580..10780,11596..11657,12371..12411,12536..12759)
/gene="F5114.3"
/note="Similar to Arabidopsis TFL1 (gb|U77674)."
/codon_start=1
/evidence=not_experimental
/protein_id="AA860904.1"
/db_xref="GI:2190540"
/translation="MSINIRDPILSVRGVDLPENRSITLKAVYGGQREVTGLDR
PSYQVNRVREIGEDIRNFYTLVMDPDPSPSNPLRLRYLHMLVDIATGTGFG
NEIYCNPSPTAGIHRVVFLEFQLGRQTVVAPGWRQNTREFABYINLGLPVAAV
FYNGQREGCGGRRL"
36957..37445
/gene="F5114.4"
join(36957..37065,37294..37445)
/gene="F5114.4"
/codon_start=1
/evidence=not_experimental
/protein_id="AA860905.1"
/db_xref="GI:2190541"
/translation="MGKSPNIAFMLPLLLIFLTSSQKLVVESTGRLKAWGFGTP
IVYTPPSRSGTSPAVFTSKMRPRPCRLPPSGYIPASDSP"
complement(40241..40963)
/gene="F5114.5"
complement(40241..40963)
/gene="F5114.5"
/codon_start=1
/evidence=not_experimental
/protein_id="AA860906.1"
/db_xref="GI:2190542"
/translation="MCSLEKRDRLFLIKLNGDGEHRNLPITLDSRTINOIRSDPSF
SOSVLTITSDGKFRFSNGYDLALASNSLSYVMDAKRSIYADISIPHTIAVYTH
ASAGCTILASHDVLNKRDRGFLYMSLDLILIVPAMFVAVLIGTSGPAARDVWL
TAAKVTADVGVKMGIVDSAGAEVYEAIRKLEELVORGGDGHVYGMKRESILREV
LIHTIGEYSGSVYRSTGSKL"
complement(41498..42875)
/gene="F5114.6"
complement(join(41498..41562,41619..41734,41808..41896,
41981..42127,42220..42267,42316..42564,42795..42875))
/gene="F5114.6"
/note="EST gb|N37484 comes from this gene."
/codon_start=1
/evidence=not_experimental
/protein_id="AA860907.1"
/db_xref="GI:2190543"
/translation="MAGRLPEEAVQATLSSLPDEVVDYVEEEEBEEMAKKESA
SSQKDALDEMASTAKDANEOAKATLEKHEQCELSRALAVLASVVRLLTTSF
ILPGLVRSVMSEREFLTKLYKVEDVYNSVEGKGGDEEDAKARALAREDSRRA
OKAIAIDKTSALDRVETMLKLEKEDIDVDNKGNNRLLRDSVDYDQVSPDEVAL
AATLKDTLKEGQELIOLNSKDKVYVVRMONTGSRLESESRD"
complement(42975..44922)
/gene="F5114.7"
complement(join(42975..43043,43213..43339,43501..43593,
43683..43771,43856..44002,44168..44480,44564..44922))
/gene="F5114.7"
/note="Similar to Saccharomyces hypothetical protein
P9642.2 (gb|U40828)."
/codon_start=1
/evidence=not_experimental
/protein_id="AA860908.1"
/db_xref="GI:2190544"
/translation="MEGFYSRLIOSPSFNGVILLPPLGRLVFOGMYSSLATA
NKPDKKGERVTSQTEASPEBCDEVEGSLAKAKAKAKLEESQSDISITQRRV
LFLGLGIPALRAIASMSREDMAKRLRMKDEPSTLQHWGKRLMLADVARIIVYRL
KLANGKLSRREQLRTYADIFRLPVAVFIIIVPMELLPFLFLPNNMLPSTFG
DKMKEBALKRLRNARMEYAKFLQDTVYKEMAKEVQTSRSGIKKTABDLQGFMTKYR.

gene
 CDS
 complement(47061..49870)
 /gene="F5114.8"
 complement(join(47061..47422,47541..47632,47766..47824,47929..48015,48122..48218,48320..48325,48704..48799,48884..48959,49053..49153,49242..49418,49467..49532,49587..49654,49750..49870))
 /gene="F5114.8"
 /note="Similar to Zea mays permease 1 (gb|U43034)." /codon_start=1
 /evidence=not_experimental
 /protein_id="AAB60909.1"
 /db_xref="GI:2190545"
 /translation="MTNGSGGNNGANRTEELQPHVKEQLQIOCVNSPPMLEAVVLGFQHYLSLGLIVLPSMLETFFEFEEFRRSLIFEFKEKVIQTLFVGLTTLFQSEFGRPLVIAVASYAIIPTSLIISRPYVDPDEPRFVTRSTOGALITGCEVLICILGVNRIIVRPLSLAPLATFGLGLYHGFPLIYNNMOTSFIDLARCEVGLPGLILFVQYLPRLPKMKGMIDGSCDRGMILICIPLVWLAQLLTS SGVDKSHHTQTSCTDRDGLITNTPWYIPYQWGSPTFIDISFAMMAASVTLFESTGLFASARYGSATPIPSVSRGTCMLGVGLNGLGIGITSTTNVGLA MTKISRIVIOISAFMIEFSIFGKGAEPASIPPLIMASIVCIYICFVCKFSFHHI CSAISINICFTEFPKIKSNSTYMAVGLSLQFCNLNENIKRILIGSFPMALISIP OYFREYVNGRSDHSHSNVSTISITL"
 complement(50678..52743)
 /gene="F5114.9"
 complement(join(50678..51059,51406..51488,51567..51733,51818..52033,52078..52294,52510..52743))
 /gene="F5114.9"
 /note="Strong similarity to Arabidopsis zeta-crystallin-like protein (gb|249268)." /codon_start=1
 /evidence=not_experimental
 /protein_id="AAB60917.1"
 /db_xref="GI:2190553"
 /translation="MGEVSVENKRVILKNTVDIPETTDMEKLGENTIEKAPRGSSRCFLVNLISCDPYRGRMRDFHSGYLPPEPGOCCELRVLEIGELFIEEEMRCRCIYALERSCTPFRCEDEWYIYMLRKLICYLLVLEIFENSLITDSFVLMRIEGLGARVIDSDPTNKPQDIVSGIIGMEERYLIRSDNLQRLNIDDDPIYSLGLIGMAGFTAVAGFNETICPKRGDSVFAACGAGVGLQGLATLHCQYVAGSGSK OKVELIKNEIICYDAFNKREKENDDTAKRRFPESIDTIFPDVNGSMIDAILNKVR GRALGVNDSLSSTSSOGINKLTSATYKRLRLEGFQSDLHLHPFLEVNKRYRK EGKIYVDSIEBGLAPALVGLFSGKNICKQVYVRAKE"
 complement(53168..54916)
 /gene="F5114.10"
 complement(join(53168..5386,53596..54114,54461..54916))
 /gene="F5114.10"
 /note="Strong similarity to Solanum polygalacturonase precursor (gb|U23053)." /codon_start=1
 /product="F5114.10"
 /protein_id="AAB60920.1"
 /db_xref="GI:2190556"
 /translation="MAELFVQVFSYITITIMSHFGPDARTSLNLSFGANPGIVESAKAFSDAMPACGVEDSVVIVPKRYLVSGEVRFGESCKREITRLRIDGLIGP QDYLGRKENMFSSGVHNTVLGSGDSITLMSKANGYCNPEGATLRFEMDSN NVKIKGVLSNLSOLFHLINRCNRKIDVRLIADPESNPTGHIHIOSTLEVNAS IKTGDDCISIGPTGNLMDVITGCGHGHSIGLSAKSIEQGVENVVKNVAVPVRT NGIRKSPRHSNGFVERVRLGAMVNVSPILIDONTCRGDSCTPQESGKIKNDY IYSGIMGSAIEIAIKDCSERVPGTGRMOWINILTSIGEAKTSCITVNSGKQLGLVT

Query Match 54.4%; Score 466; DB 8; Length 109560;
 Best Local Similarity 100.0%; Pred. No. 8.3e-100;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 366 GGCAATGAGATTGTGTAGCAAAATCCCAAGTCCAGTGAAGATTGCTGTGCTG 425
 |||||||
 DB 12535 GGCAATGAGATTGTGTAGCAAAATCCCAAGTCCAGTGAAGATTGCTGTGCTG 12594
 |||||||

OY 426 TTATATGTTTCGACAGCTGGCAGCAAAAGATGATGCACAGGCGGCCAGAAC 485
 |||||||
 DB 12595 TTATATGTTTCGACAGCTGGCAGCAAAAGATGATGCACAGGCGGCCAGAAC 12654
 |||||||

OY 486 TTCACACTCGCAGATTGCTGAGATCTACAAATCTCGGCTTCCCGTGGCCGAGTTTC 545
 |||||||
 DB 12655 TTCACACTCGCAGATTGCTGAGATCTACAAATCTCGGCTTCCCGTGGCCGAGTTTC 12714
 |||||||

OY 546 TACAAATGTCAGAGGAGAGAGTGGCTCGGAGNAGAACTTAAATGCTTCTCTTT 605
 |||||||
 DB 12715 TACAAATGTCAGAGGAGAGTGGCTCGGAGNAGAACTTAAATGCTTCTCTTT 12774
 |||||||

OY 606 ATACCAATGATATGATGATCTGATGATGATTTATGATCATGATATTTAAATTTAA 665
 |||||||
 DB 12775 ATACCAATGATATGATGATCTGATGATGATTTATGATCATGATATTTAAATTTAA 12834
 |||||||

OY 666 TAACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
 |||||||
 DB 12835 TAACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12894
 |||||||

OY 726 GTGTGTAAATAAATAGAGGGGAGAGAAATGAGAGTGTTTACTATATAGTGTGTA 785
 |||||||
 DB 12895 GTGTGTAAATAAATAGAGGGGAGAGAAATGAGAGTGTTTACTATATAGTGTGTA 12954
 |||||||

OY 786 TGGGAT 831
 |||||||
 DB 12955 TGGGAT 13000
 |||||||

RESULT 9
 AF152096 2483 bp DNA linear PLN 22-DEC-1999
 LOCUS Arabidopsis thaliana flowering locus T (FT) gene, complete cds.
 DEFINITION AF152096
 ACCESSION AF152096.1 GI:6117977
 KEYWORDS
 SOURCE
 ORGANISM Arabidopsis thaliana.
 Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 2483)
 Kardalisky, I., Shukla, V. K., Ahn, J. H., Degenais, N., Christensen, S. K., Nguyen, J. T., Chory, J., Harrison, M. J. and Weigel, D.
 Activation tagging of the floral inducer FT
 Science 286 (5446), 1962-1965 (1999)
 MEDLINE 20050959
 PUBMED 10583961
 TITLE 2 (bases 1 to 2483)
 JOURNAL Kardalisky, I. and Weigel, D.
 DIRECT SUBMISSION
 TITLE Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 JOURNAL

FEATURES
 source location/Qualifiers
 1..2483
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="1"
 /map="90 cM; F5114"
 1..2483
 /gene="FT"
 join(1..264,1080..1141,1855..1895,2020..2483)
 /gene="FT"
 /product="flowering locus T"
 1..63
 /gene="FT"
 join(64..264,1080..1141,1855..1895,2020..2243)
 /gene="FT"
 /function="induces flowering"
 /note="similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PEBP) and Raf kinase inhibitor protein;
 corresponds to Arabidopsis thaliana BAC F5114 sequence

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 02:33:53 ; Search time 282.5 Seconds
(without alignments)
6823.754 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856

Sequence: 1 tctaagaactagtgtatcccc.....aaaaaaaaaaaaactgcgag 856

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	856	100.0	856	AAZ28490	Flowering locus T
2	856	100.0	856	AAZ28491	Flowering locus T
3	692.4	80.9	775	AAC34682	Arabidopsis thaliana
4	692	80.8	754	AAC48359	Arabidopsis thaliana
5	528	61.7	528	AAA60683	Arabidopsis thaliana
6	377.6	44.1	528	AAC42966	Arabidopsis thaliana
7	374.4	43.7	528	AAA60684	Arabidopsis thaliana
8	180.2	21.1	522	AAC90636	Strawberry flower1
9	176.8	20.7	668	AAI60140	Arabidopsis termin

10	176	20.6	762	24	ABK82093	Novel floral meris
11	176	20.6	792	24	ABK82091	DNA encoding novel
12	176	20.6	792	24	ABK82092	DNA encoding novel
13	176	20.6	1225	24	ABK82122	DNA encoding novel
14	175	20.4	787	22	ABK82094	Novel floral meris
15	161.2	18.8	519	22	AAC90668	Strawberry flower1
16	145.8	17.0	4512	19	AAV66749	Arabidopsis pathog
17	116	13.6	929	18	AAI60139	Antirrhinum centro
18	82.6	9.6	3696	22	AAC90666	Strawberry flower1
19	80	9.3	1430	18	AAI60142	Arabidopsis termin
20	71.8	8.4	822	12	AAQ14832	OV-16 antigen. On
21	63	7.4	4952	22	AAC90667	Strawberry flower1
22	55.6	6.5	567	24	ABO55599	Human ovarian anti
23	52.8	6.2	2426	22	AAI17465	Splachn lycopene e
24	51.8	6.1	1637	20	AAI30973	Porcine complement
25	51.2	6.0	970	24	ABN73995	Bovine embryonic g
26	51	6.0	988	24	ABN74181	Bovine embryonic g
27	50.2	5.9	557	22	AAH35052	Bovine colon cancer
28	50.2	5.9	18585	24	ABL34609	Human metastasis a
29	50	5.8	649	22	AAK60828	Human immune/haema
30	49.2	5.7	503	23	ABK41982	CDNA encoding nove
31	49.2	5.7	925	24	ABN74030	Bovine embryonic g
32	49.2	5.7	978	22	ABN77091	Proliferative glom
33	49.2	5.7	83391	24	ABO67094	Human angiogenesis
34	49	5.7	1012	22	ABA77106	Proliferative glom
35	48.8	5.7	956	24	ABN74279	Bovine embryonic g
36	48.8	5.7	2637	24	AAI34120	Human secreted pro
37	48.6	5.7	427	24	ABO54500	Human ovarian anti
38	48.6	5.7	745	22	AAK62481	Human immune/haema
39	48.4	5.7	789	24	ABK28390	DNA transcription
40	48.2	5.6	367	22	AAI28106	Novel cDNA encodin
41	48.2	5.6	939	22	ABN74051	Bovine embryonic g
42	48	5.6	551	21	AAI16381	Human prostate can
43	48	5.6	654	22	AAH34361	Human colon cancer
44	48	5.6	910	24	ABN73980	Bovine embryonic g
45	48	5.6	910	24	ABN73981	Bovine embryonic g

ALIGNMENTS

RESULT 1		
ID	AAZ28490	standard; cDNA; 856 BP.
AC	AAZ28490;	
XX		
DT	17-JAN-2000	(first entry)
XX		
DE	Flowering locus T (FT) gene.	
XX		
KW	Flowering locus T gene; FT; flowering time; modulator; early flowering;	
KW	antibody; cellular binding protein; crop; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	63..590
FT		/*tag= a
FT		/product= FT
XX		/note= "Flowering locus T"
XX		
PN	W09953070-A1.	
XX		
PD	21-OCT-1999.	
XX		
PF	13-APR-1999;	99MO-US08151.
XX		
PR	15-APR-1998;	98US-0060726.
XX		
PA	(SALK) SALK INST BIOLOGICAL STUDIES.	
XX		
PI	Weigel D;	

xx WPI: 1999-611305/52.
DR P-PSDB: AMV49098.
xx
FT New flowering locus T polypeptide that regulates flowering time,
PT particularly used to accelerate flowering
xx
PS Claim 5; Fig 2; 64pp; English.
xx
CC This sequence is the flowering locus T (FT) gene of *Arabidopsis thaliana*.
CC FT regulates flowering in plants by modulating flowering time.
CC Overexpression of FT results in early flowering, while loss of function
CC mutations or antisense directed to FT causes late flowering. The FT
CC polypeptide has a molecular weight of approximately 20kD, and is located
CC on chromosome 1. The FT polypeptide is used in the invention to modulate
CC flowering time in many mono and dicotyledonous plants. The FT
CC polynucleotide sequence is used for recombinant production of the
CC polypeptide, and as a source of antisense, ribozyme or triplex forming
CC sequences. The FT polypeptide can also be used to raise antibodies and to
CC screen for modulators or cellular binding proteins. The methods of the
CC invention allow for the production of crops at any time of year.
xx
SQ Sequence 856 BP; 263 A; 150 C; 194 G; 249 T; 0 other;

Query Match	100.0%	Score 856:	DB 20:	Length 856:
Best Local Similarity	100.0%	Pred. NO. 3.8e-150;		
Matches 856:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY - 1	TC TAGA CTA GTAGT AGTCCCGCGGCTGCAGAGAAATTCAGCAGCAGAGGTTGTTCAAGATCA	60		
Db 1	TC TAGA CTA GTAGT AGTCCCGCGGCTGCAGAGAAATTCAGCAGCAGAGGTTGTTCAAGATCA	60		
QY 61	AGATGCTATATAATTTAAGACACCTCTTATATGTAAGCAGAGTGTGGACAGCTTCTTG	120		
Db 61	AGATGCTATATAATTTAAGACACCTCTTATATGTAAGCAGAGTGTGGACAGCTTCTTG	120		
QY 121	ATCCGTTTAATATGATCAATCACTCAAAAGGTTACTATGAGGCCAAAGAGAGGATGTAATG	180		
Db 121	ATCCGTTTAATATGATCAATCACTCAAAAGGTTACTATGAGGCCAAAGAGAGGATGTAATG	180		
QY 181	GCTTGGAATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAAAGATGTAAGTGTGGAGAG	240		
Db 181	GCTTGGAATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAAAGATGTAAGTGTGGAGAG	240		
QY 241	ACCTGAGGAACTTCTATACCTTGGTTATGTTGATGCCAGATGTTCCAAAGTCTAGCAAC	300		
Db 241	ACCTGAGGAACTTCTATACCTTGGTTATGTTGATGCCAGATGTTCCAAAGTCTAGCAAC	300		
QY 301	CTCACCCTCGAAGATATCTCCATGGTGGTGGTACTGATATCCCTGCTCAATGGAACAA	360		
Db 301	CTCACCCTCGAAGATATCTCCATGGTGGTGGTACTGATATCCCTGCTCAATGGAACAA	360		
QY 361	CCTTTGGCAATGAGATGTGTGTACGAAAAATCCAAAGTCCCACTCAGAGAAATTCATCGT	420		
Db 361	CCTTTGGCAATGAGATGTGTGTACGAAAAATCCAAAGTCCCACTCAGAGAAATTCATCGT	420		
QY 421	TGCGTTTATATATGTTTGCGACGCTTGCGCAGGCAAAAGTGTATGACCAGGCGGCGC	480		
Db 421	TGCGTTTATATATGTTTGCGACGCTTGCGCAGGCAAAAGTGTATGACCAGGCGGCGC	480		
QY 481	AGAACTTCAACACTGCGCAGTTTGTGAGATCTACAATCTGGGCGCTTCCGTTGCGCAG	540		
Db 481	AGAACTTCAACACTGCGCAGTTTGTGAGATCTACAATCTGGGCGCTTCCGTTGCGCAG	540		
QY 541	TTTTTCACAATTTGTAGAGGGAGAGTGGCTGGCGGAGGAAGACTTTAGATGGCTCTT	600		
Db 541	TTTTTCACAATTTGTAGAGGGAGAGTGGCTGGCGGAGGAAGACTTTAGATGGCTCTT	600		
QY 601	CCTTATATAACCAATTGATATTTGCATATCTGTATGAGATTTATGCATCTATAGTATTTAA	660		
Db 601	CCTTATATAACCAATTGATATTTGCATATCTGTATGAGATTTATGCATCTATAGTATTTAA	660		
QY 661	TTTATATACCAATTTATGATACGAGTAACGAACGGTATGATGCTATAGTAGTTCAATA	720		

Dd	661	TTTATTAACCACTTTATTATATGAGGTAAAGAACGGTGATGATGGCTATTAGTAGTCATA	720
Oy	721	TATTAAGTGTGTAATAAAAATGAGGGGGAGAAAATGACAGCTTTTACTTATATAGTG	780
Dd	721	TATAAGGTGTGAATAAAAATGAGGGGGAGAAAATGAGAGCTTTTACTTATATAGTG	780
Oy	781	TGTGATGCATATATATTTATCTACATCAATGAATGAAGTGTATATTTATTAAAAAAAAAA	840
Dd	781	TGTGATGCCATATATTTATCTACATCAATGAATGAAGTGTATATTTATTAAAAAAAAAA	840
Oy	841	AAAAAAAAAACTCGAG 856 	
Dd	841	AAAAAAAAAACTCGAG 856	

RESULT 2
 AAZ28491/C
 ID AAZ28491 standard: CDNA, 856 BP.
 XX
 AC AAZ28491;
 DT 17-JAN-2000 (first entry)
 XX
 DE Flowering locus T (FT) gene antisense insert.
 XX
 KM Flowering locus T gene; FT: flowering time; modulator; early flowering;
 XX antibody; cellular binding protein; crop; antisense construct; ss.
 OS Arabidopsis thaliana.
 XX
 PN W09953070-A1.
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US08151.
 XX
 PR 15-APR-1998; 98US-0060726.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Weigel D;
 XX
 DR WPI: 1999-611305/52.
 XX
 PT New flowering locus T polypeptide that regulates flowering time,
 PT particularly used to accelerate flowering -
 XX
 PS Example 2; Fig 3; 64pp; English.
 CC
 CC This is the flowering locus T (FT) gene antisense polynucleotide
 CC sequence. This sequence is used in the production of the antisense
 CC construct of the invention pSKR1060. FT regulates flowering in plants by
 CC modulating flowering time. Overexpression of FT results in early
 CC flowering, while loss of function mutations or antisense directed to FT
 CC causes late flowering. The FT polypeptide has a molecular weight of
 CC approximately 20kD, and is located on chromosome 1. The FT polypeptide is
 CC used in the invention to modulate flowering time in many mono and
 CC di-cotyledonous plants. The FT polynucleotide sequence is used for
 CC recombinant production of the polypeptide, and as a source of antisense,
 CC ribozyme or triplex forming sequences. The FT polypeptide can also be
 CC used to raise antibodies and to screen for modulators or cellular binding
 CC proteins. The methods of the invention allow for the production of crops
 CC at any time of year.
 CC
 SO Sequence 856 BP; 249 A; 194 C; 150 G; 263 T; 0 other;
 XX
 XX
 Query Match 100.0%; Score 856; DB 20; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3,8e-190;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 TCTAGACTAGTGTGATCCCGCGGCTGCAGAGATTTCACACAGAGTTTGTTCACAGATCAA 60

Db 856 TCTAGACTAGTGGATCCCGGGGCTGCAGAAATTCAGCAGGAGTTTGTTCAGATCAA 797
OY 61 AGATGCTAATAATTAAGACCCCTCTATTAGTAAAGCAGAGTTGGAGAGCTTCTTG 120
Db 796 AGATGCTAATAATTAAGACCCCTCTATTAGTAAAGCAGAGTTGGAGAGCTTCTTG 737
OY 121 ATCCGTTTAAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGTACTAATG 180
Db 736 ATCCGTTTAAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGTACTAATG 677
OY 181 GCTTGATCTAAGCCCTTCTCAGGTTCAAAACCAAGAGTTGAGATTGGTGAGAG 240
Db 676 GCTTGATCTAAGCCCTTCTCAGGTTCAAAACCAAGAGTTGAGATTGGTGAGAG 617
OY 241 ACCTCAGGAACCTCTAATCTTGGTATGGTATGATCCAGATGTTCCAAAGTCCAGAAC 300
Db 616 ACCTCAGGAACCTCTAATCTTGGTATGGTATGATCCAGATGTTCCAAAGTCCAGAAC 557
OY 301 CTCACCTCGAGAAATATCTCCATTGGTGTGACTGATATCCCTGCTACAACTGAAACAA 360
Db 556 CTCACCTCGAGAAATATCTCCATTGGTGTGACTGATATCCCTGCTACAACTGAAACAA 497
OY 361 CCTTGGCAATGAGATTGTGTGTACGAAATCCAAAGTCCCACTGCAAGATTCATCTG 420
Db 496 CCTTGGCAATGAGATTGTGTGTACGAAATCCAAAGTCCCACTGCAAGATTCATCTG 437
OY 421 TCGTGTATATTTGTTCAGACCTTGGCAGGAAACAGTATGCAACCGGTTGGGCC 480
Db 436 TCGTGTATATTTGTTCAGACCTTGGCAGGAAACAGTATGCAACCGGTTGGGCC 377
OY 481 AGAAGCTTCAACCTCGAGTTTGTGAGATCTACAATCTCGGCTCCCGTGCGCCAG 540
Db 376 AGAAGCTTCAACCTCGAGTTTGTGAGATCTACAATCTCGGCTCCCGTGCGCCAG 317
OY 541 TTTTTCACAAATTTGTCAAGAGGAGAGTGCGTCCGAGAGAGACATTAGATGGCTCTT 600
Db 316 TTTTTCACAAATTTGTCAAGAGGAGAGTGCGTCCGAGAGAGACATTAGATGGCTCTT 257
OY 601 CCTTATTAACCATTAATATGATCTGATCTGAGATTAATGATTAATGATTAATTTAA 660
Db 256 CCTTATTAACCATTAATATGATCTGATCTGAGATTAATGATTAATGATTAATTTAA 197
OY 661 TTTAATTAACCATTTTATGATAGAGTAACGAGTATGATCCCTATAGTATTCATA 720
Db 196 TTTAATTAACCATTTTATGATAGAGTAACGAGTATGATCCCTATAGTATTCATA 137
OY 721 TATTAAGTGTATTAATAAATGAGAGGGGAGAAATGAGAGTGTACTTATATAGTG 780
Db 136 TATTAAGTGTATTAATAAATGAGAGGGGAGAAATGAGAGTGTACTTATATAGTG 77
OY 781 TGTGATGCGTATTTATTTATATCTACATGAATGAAGTGTATTTATTAATAAAAAA 840
Db 76 TGTGATGCGTATTTATTTATATCTACATGAATGAAGTGTATTTATTAATAAAAAA 17
OY 841 AAAAAAAAAAATCTGAG 856
Db 16 AAAAAAAAAAATCTGAG 1
RESULT 3
AAC34682
ID AAC34682 standard; DNA; 775 BP.
XX AAC34682;
AC
AC 17-OCT-2000 (first entry)
DT
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7506.
XX
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX

OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141844.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144684.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145224.
 PR 23-JUL-1999; 99US-0145228.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145291.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157153.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
 Best Local Similarity 99.9%; Pred. No. 5,3e-152;
 Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 45 GTTGTTCAGATCAAGATGCTTAATAATATAGAGACCCCTTATAGTAGAGAGCTT 104
 DB 65 GTTGTTCAGATCAAGATGCTTAATAATATAGAGACCCCTTATAGTAGAGAGCTT 124
 QY 105 GTTGAGACGTTCTGATCCGTTTATATAGATCAATCACTCTTAAGGTTACTTATAGGCCAA 164
 DB 125 GTTGAGACGTTCTGATCCGTTTATATAGATCAATCACTCTTAAGGTTACTTATAGGCCAA 184
 QY 165 AGAGAGGTGACTAATGCTTGAATAGAGCCCTTCAAGGTTCAAAACAGCAAGAGTT 224
 DB 185 AGAGAGGTGACTAATGCTTGAATAGAGCCCTTCAAGGTTCAAAACAGCAAGAGTT 244
 QY 225 AGATTTGTGAGAGAGACCTCAGAACTCTATACTTTGGTTATGTTGATCCAGATGTT 284
 DB 245 GAGATTTGTGAGAGAGACCTCAGAACTCTATACTTTGGTTATGTTGATCCAGATGTT 304
 QY 285 CCAAGTCTAGACACCCCTCAGCAATATCTCCATTGGTTGGTACTGATATCCCT 344
 DB 305 CCAAGTCTAGACACCCCTCAGCAATATCTCCATTGGTTGGTACTGATATCCCT 364
 QY 345 GCTACACTGAGACAACTTTGGCAATGAGATTGTTGAGAAATCCAGTCCACT 404
 DB 365 GCTACACTGAGACAACTTTGGCAATGAGATTGTTGAGAAATCCAGTCCACT 424
 QY 405 GCAGGAATTCATGCTGTGTTTATATGTTTGCACAGCTTGCAGGCAACAGTGTAT 464

Db	425	GCAGGAATTCATCGTGTGTCGTTTAAATTTGTTTCGACACCTTGGGAGCCAAACAGTGTAT	484
Qy	465	GCACACAGGTGGCCGCAGAACTTCACACACTGCGAGTTTGCTGAGATCTCAATCTCGGC	524
Db	485	GCACACAGGTGGCCGCAGAACTTCACACACTGCGAGTTTGCTGAGATCTCAATCTCGGC	544
Qy	525	CTTCCCGTGGCCGCAAGTTTCTACAAATGTCAGAGGAGAGTGGCTCGGAGGAAGA	584
Db	545	CTTCCCGTGGCCGCAAGTTTCTACAAATGTCAGAGGAGAGTGGCTCGGAGGAAGA	604
Qy	585	CTTTAGATGGCTCTCTCCTTTATACCAATGTGATGCACTCTGATAGATTTATGC	644
Db	605	CTTTAGATGGCTCTCTCCTTTATACCAATGTGATGCACTCTGATAGATTTATGC	664
Qy	645	ATCTATAGTATTTAAATTAATTAACCACTTTTATGATACGAGTAACGAACGGTATGATGC	704
Db	665	ATCTATAGTATTTAAATTTATTAATTAACCACTTTTATGATACGAGTAACGAACGGTATGATGC	724
Qy	705	CTATAGTAGTTCCAATTAATTAAGTGTGTAATAAA	738
Db	725	CTATAGTAGTTCCAATTAATTAAGTGTGTAATAAA	758
RESULT 4			
AAC48359			
ID	AAC48359 standard; DNA; 754 BP.		
XX			
AC	AAC48359;		
XX			
DT	18-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EPI033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128224.	
PR	08-APR-1999;	99US-0128714.	
PR	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
PR	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
PR	28-APR-1999;	99US-0130891.	
PR	30-APR-1999;	99US-0131449.	
PR	30-APR-1999;	99US-0132048.	
PR	30-APR-1999;	99US-0132407.	
PR	04-MAY-1999;	99US-0132404.	
PR	05-MAY-1999;	99US-0132485.	
PR	06-MAY-1999;	99US-0132486.	
PR	06-MAY-1999;	99US-0132487.	
PR	07-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	
PR	14-MAY-1999;	99US-0134291.	
PR	14-MAY-1999;	99US-0134219.	
PR	14-MAY-1999;	99US-0134221.	
PR	14-MAY-1999;	99US-0134370.	
PR	18-MAY-1999;	99US-0134768.	

PR	19-MAY-1999	9905-0134941
PR	20-MAY-1999	9905-0135124
PR	21-MAY-1999	9905-0135523
PR	24-MAY-1999	9905-0135629
PR	25-MAY-1999	9905-0136021
PR	27-MAY-1999	9905-0136392
PR	28-MAY-1999	9905-0136782
PR	01-JUN-1999	9905-0137222
PR	03-JUN-1999	9905-0137528
PR	04-JUN-1999	9905-0137502
PR	07-JUN-1999	9905-0137724
PR	08-JUN-1999	9905-0138094
PR	10-JUN-1999	9905-0138540
PR	10-JUN-1999	9905-0138847
PR	14-JUN-1999	9905-0139141
PR	16-JUN-1999	9905-0139452
PR	16-JUN-1999	9905-0139453
PR	17-JUN-1999	9905-0139462
PR	18-JUN-1999	9905-0139454
PR	18-JUN-1999	9905-0139455
PR	18-JUN-1999	9905-0139456
PR	18-JUN-1999	9905-0139457
PR	18-JUN-1999	9905-0139458
PR	18-JUN-1999	9905-0139459
PR	18-JUN-1999	9905-0139460
PR	18-JUN-1999	9905-0139461
PR	18-JUN-1999	9905-0139462
PR	18-JUN-1999	9905-0139463
PR	18-JUN-1999	9905-0139750
PR	18-JUN-1999	9905-0139763
PR	21-JUN-1999	9905-0139817
PR	22-JUN-1999	9905-0139869
PR	23-JUN-1999	9905-0140353
PR	23-JUN-1999	9905-0140354
PR	24-JUN-1999	9905-0140695
PR	28-JUN-1999	9905-0140823
PR	29-JUN-1999	9905-0140991
PR	30-JUN-1999	9905-0141287
PR	01-JUL-1999	9905-0141842
PR	01-JUL-1999	9905-0142154
PR	02-JUL-1999	9905-0142055
PR	06-JUL-1999	9905-0142390
PR	08-JUL-1999	9905-0142803
PR	09-JUL-1999	9905-0142920
PR	12-JUL-1999	9905-0142977
PR	13-JUL-1999	9905-0143542
PR	14-JUL-1999	9905-0143624
PR	15-JUL-1999	9905-0144005
PR	16-JUL-1999	9905-0144085
PR	16-JUL-1999	9905-0144325
PR	19-JUL-1999	9905-0144386
PR	19-JUL-1999	9905-0144311
PR	19-JUL-1999	9905-0144332
PR	19-JUL-1999	9905-0144333
PR	19-JUL-1999	9905-0144334
PR	19-JUL-1999	9905-0144335
PR	21-JUL-1999	9905-0144518
PR	21-JUL-1999	9905-0145086
PR	21-JUL-1999	9905-0145085
PR	22-JUL-1999	9905-0145085
PR	22-JUL-1999	9905-0145087
PR	22-JUL-1999	9905-0145089
PR	22-JUL-1999	9905-0145192
PR	23-JUL-1999	9905-0145145
PR	23-JUL-1999	9905-0145148
PR	23-JUL-1999	9905-0145224
PR	26-JUL-1999	9905-0145276
PR	27-JUL-1999	9905-0145373
PR	27-JUL-1999	9905-0145519
PR	27-JUL-1999	9905-0145519

PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159350.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 14-OCT-1999; 99US-0159658.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.

PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 80.8%; Score 692; DB 21; Length 754;
 Best Local Similarity 100.0%; Pred. No. 6,5e-152;
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 GTTGTCAAGATCAAGATGCTATTAATATAGAGACCTCTATATGTAAGAGACTT 104
 DB 63 GTTGTCAAGATCAAGATGCTATTAATATAGAGACCTCTATATGTAAGAGACTT 122
 OY 105 GTTGAGAGCTTGTGATCCGTTTATGATCAATCACTCAAGAGTACTTATGCGCAA 164
 DB 123 GTTGAGAGCTTGTGATCCGTTTATGATCAATCACTCAAGAGTACTTATGCGCAA 182
 OY 165 AGAGAGTGACTAATGCGTGGATCTAAGCGCTTCTCAGTTCAAAACAGCAAGACTT 224
 DB 183 AGAGAGTGACTAATGCGTGGATCTAAGCGCTTCTCAGTTCAAAACAGCAAGACTT 242
 OY 225 GAGATTGCTGAGAAAGACCTCAGAACTTCTATACTTTGTTTANGTGATCCAGATGTT 284
 DB 243 GAGATTGCTGAGAAAGACCTCAGAACTTCTATACTTTGTTTANGTGATCCAGATGTT 302
 OY 285 CCAAGTCCAGAACCCCTCAGATATCTCCATGTTGGTGGTACTGATATCCCT 344
 DB 303 CCAAGTCCAGAACCCCTCAGATATCTCCATGTTGGTGGTACTGATATCCCT 362
 OY 345 GCTACAACTGAGAACACCTTTGGCAATGAGATTGTTGTACGAATAATCAAGTCCACT 404
 DB 363 GCTACAACTGAGAACACCTTTGGCAATGAGATTGTTGTACGAATAATCAAGTCCACT 422
 OY 405 GCAGAAATTCATCGTGTGTTTATATGTTTGCAGACGTTTGCAGAGCAACAGTGTAT 464
 DB 423 GCAGAAATTCATCGTGTGTTTATATGTTTGCAGACGTTTGCAGAGCAACAGTGTAT 482
 OY 465 GCACAGAGTGCGCCGACAGACTTCACACCTGCGAGTTTGGTGCATACAACTCGGC 524
 DB 483 GCACAGAGTGCGCCGACAGACTTCACACCTGCGAGTTTGGTGCATACAACTCGGC 542
 OY 525 CTTCCTGCGCGCGAGTTTCTACAAATGTCAGAGGAGAGTGGCTGGGAGAAAGA 584
 DB 543 CTTCCTGCGCGCGAGTTTCTACAAATGTCAGAGGAGAGTGGCTGGGAGAAAGA 602
 OY 585 CTTTATGATGCGCTTCTCTTATTAACCAATGATATTCATACCTGTGATGATTTATGC 644
 DB 603 CTTTATGATGCGCTTCTCTTATTAACCAATGATATTCATACCTGTGATGATTTATGC 662
 OY 645 ATCTATGATATTTTAAATTAATTAACCAATTTATGATAGAGTAAGAGAGTGTATGATGC 704
 DB 663 ATCTATGATATTTTAAATTAATTAACCAATTTATGATAGAGTAAGAGAGTGTATGATGC 722
 OY 705 CTATAGTAGTTCAATATATTAAGTGTATATA 736
 DB 723 CTATAGTAGTTCAATATATTAAGTGTATATA 754

RESULT 5
 AAA60683 standard; DNA; 528 BP.
 ID AAA60683;
 AC AAA60683;
 XX
 DT 26-OCT-2000 (first entry)
 DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.
 XX Arabidopsis thaliana; Cruciferae; plant; control; flowering;
 KW solar radiation; ds.
 XX

PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 29-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142820.
PR 13-JUL-1999; 99US-0142877.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 15-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149175.
PR 20-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151086.
PR 27-AUG-1999; 99US-0151087.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0156559.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 44.1%; Score 377.6; DB 21; Length 528;
Best local Similarity 82.2%; Pred. No. 1.2e-78;
Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 63 AAGCTATAAATATAGAGACCCCTTATATAGAGAGAGTGTGGAGAGCTTCTGAT 122
DB 1 AATGCTTTAAGTCGTAGAGATCCCTTGTGTCGCGAGTGTGTCAGATGTTCTTAT 60
OY 123 CCGTTAATAGATCATCTCATAGGTTACTATATGCCAAGAGAGGTGACTAATGCC 182
DB 61 CCTTCACGAGGTGTGCTCTTAAAGTCACTATAGAGCATAGAGAGGTACTAATGAC 120
OY 183 TTGATCTAAGGCTTCTAGGTTCAAAACCAAGCAAGAGTGGAGTTGGAGAGAGC 242
DB 121 TTGATCTAAGGCTTCTCAAGTTCTGAAACCAACCAATATGAGATGGAGAGAGC 180

OY	243	CTCAGGAACCTCTTACTGTTGGTATGATGGGATATCCAAATCTTCCAACTCTACCAACCTT	302
Db	181	TTTCGAAATTTCTACACCTGGTATGATGGGATATCCAAATGTCGGAATCCCAACCAACCTT	240
OY	303	CACCTCCGAGAAATATCTCCATATGGTGGTACATATATCCCTGCTACCAATCGGAACAAC	362
Db	241	CACCAACGAGAAATATCTCCATGTTGGTGGTACATATATCTGCTACCAATCGGAATATGCC	300
OY	363	TTTGGCAATGAGATTGTGTGTTTACGAAATATCCAGTCCCACTGCAGGAATTCATCTGTTC	422
Db	301	TTTGGCAATGAGGTGTGTGTCTACGAGAGTCCACAGTCCCTCCGGAATTCATCTGTATTT	360
OY	423	GTGTTTATATTGTTTCGACAGCTTGGCAGGCAAAACAGTGTATGACCAGGGGTGGCCGAC	482
Db	361	GTGTTGGAATTTGTTCCGGCACTCGGAAGCAAAACGGTTTATGACCCGGGGGTGGCCGAA	420
OY	483	AACCTTCAACACTGCGCGAGTTTGCTGGAATCTACATATCTCGGCTTCCCGTGCCGACGTT	542
Db	421	CAGTTCACAACCTCGTGGGTGGTGGCAATCTACATATTTGGTCTTCTCGTGCGCTGCCTT	480
OY	543	TTCTACAAATTCGACAGGGGAGTGGTGGGGAGAGAGAAAGACTTTT	590
Db	481	TACTTCAACTGCCAGAGGGAGAAATGGCTGTGGGGGAGAAAGAACTGTG	528

```

RESULT 7
AAA60684
ID AAA60684 standard; DNA; 528 BP.
XX
XX AAA60684;
XX
XX AC
XX DT 26-OCR-2000 (first entry)
XX DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.
XX
XX Arabidopsis thaliana; Cruciferae; plant; control; flowering;
XX
XX Arabidopsis thaliana; ds.
XX
XX Arabidopsis thaliana.
XX
XX OS Arabidopsis thaliana.
XX
XX PN JP2000139250-A.
XX
XX PD 23-MAY-2000.
XX
XX PF 11-NOV-1998; 98JP-0320219.
XX-
XX PR 11-NOV-1998; 98JP-0320219.
XX
XX PA (TORA ) TORAY IND INC.
XX
XX DR WPI; 2000-425906/37.
XX
XX PT A method to accelerate plant generation and generation accelerated
XX PT plants -
XX PS
XX PS Claim 5; Page 5; 6pp; Japanese.
XX
XX the present invention describes a method to accelerate plant generation
XX and generation accelerated plants. The method uses a controlling gene
XX functioning in the downstream of a gene under the control of solar
XX radiation to accelerate plant generation using a gene functioning to
XX accelerate the flowering time regardless of solar radiation. The method
XX can control flowering time to a desired period by shortening the
XX juvenile stage. The present sequence represents a specifically claimed
XX Arabidopsis nucleotide sequence, which is used in the exemplification
XX of the present invention.
XX
SQ Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;
Query Match 43.7%; Score 374.4; DB 21; Length 528;
Best Local Similarity 81.8%; Pred. NO. 6.9e-78;
Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps

```

OY	63	ANGTCATATAAATAAGAGACCCTCTATATAGTAGCAGACTGTGTGGAGACGTTCTTGAT	122
Db	1	ATGCTTTTAAAGTCGTAGAGATCTCTCTGTGGTGGCAGTGTGTGGAGATGTTCTTGAT	60
OY	123	CCGTTTATATGATCAATCACTCTAAAGGTAACTTAATAGCCAAAGAGAGGTCAATAGGC	182
Db	61	CGTTTCACGAGGTGGTCTCTCTTAAGTCACTTATAGCCATAGAGAGGTACTAATGCC	120
OY	183	TTTGATCTTAAGCCCTTCCAGAGTTCAAAACAGCCCAAGAGTTGAGTTGTGGAGAAC	242
Db	121	TTGGATCTAAGCCCTTCAGAGTTCTGAACAAACCAATATAGGAGATTTGAGAGGAGAC	180
OY	243	CTCAGGAACCTTCTAATTCTTGGTATGATGGATCCAGATGTTCCAGTCTTAGCAACCT	302
Db	181	TTCAGAATTTCTACACCTTGATGGTATGGATGCTATGAGCCGAGTCCAAACACCT	240
OY	303	CACCTCCGAGATATCTCCATTTGGTGGTACTATATCCCTGCTACAACTGGACAAAC	362
Db	241	CACCAACGAGATATCTCCACTGGTGGTACTGATATACCTGGCAACACTGGAAATGCC	300
OY	363	TTTGGCAATGAGATTGTGTGTAGAAATAATCCAGTCCCACTGGAGGAATTCATCGTGC	422
Db	301	TTTGGCAATGAGTGGTGGTGTCTACGAGAGTCCAGTCCCCCTCGGGAATTCATCGATT	360
OY	423	GTGTTTATATGTTTCGACACTTGGCAGAGCGAAACAGTATATGACCAAGGGTGGCGCAG	482
Db	361	GTGTTGCTATGTTTCCGGCAACTCGGAAGCAAAAGGTTTATATGCAACCGGGGTGGCGCA	420
OY	483	AACTTCAACACTCGCGAGTTTGTGAGATCTACAACTCGGCGTTCCCGTGGCGCAGTT	542
Db	421	CAGTTCACAACTCGTGAGTTTGTGAGATCTACAACTTGGTCTTCTCGTGGCGCTCT	480
OY	543	TTTACAAATTTGTCAGAGGAGAGTGGTGGCGGAGAGAAAGACTTGG	590
Db	481	TACTTCAACTCCAGAGGAGAAATGGTGTGGGGGAGAGAAACGTGG	528

```

RESULT 8
AAC90636
ID AAC90636 standard; cDNA; 522 BP.
XX
XX AAC90636;
AC
XX
DT 20-MAR-2001 (first entry)
XX
DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 5.
XX
XX Strawberry; flowering regulation; floral homeotic gene; field crop;
KW harvesting; fruit production; ss.
XX
OS Fragaria vesca.
XX
PN WO200071722-A1.
XX
PD 30-NOV-2000.
XX
PE 24-MAY-2000; 2000WO-US14297.
XX
PR 25-MAY-1999; 99US-0318789.
PR 24-MAY-2000; 2000US-0318789.
XX
PA (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX
PI Oeller P, Guttererson N;
XX
XX WPI: 2001-025165/03.
DR P-PSDB: AAB50266.
XX
PT Novel nucleic acid involved in controlling plant flowering processes
PT useful for generating transgenic plants, in particular strawberry
PT plants having altered flowering behavior such as early, delayed or
PT day-neutral flowering
XX

```


DB 382 TTGTGTTTGTTCGTCAGCAGCAAGACGTGTATCTTCCATATTCCTTCG 441
OY 477 CGCCAGAACTTCAACACTCGCGAGTTGCTGATCTACAAATCTCGCCTCCGTCGCC 536
DB 442 AGAATGATCACTTCAACACTCGTAATTTGCGCTGAGTGTATGTCCTCCGTCGCCG 501
OY 537 GCAGTTTCTCAATTTGTCACAGGAGA 564
DB 502 GCCGCTTCTTAAAGCAAGAGAGAA 529

RESULT 10
ABR82093
ID ABR82093 standard; cDNA: 762 BP.
AC ABR82093;
XX
DT 27-AUG-2002 (first entry)
XX
DE Novel floral meristem identity gene *LpCENa* contig #2.
XX
KW Ryegrass; fescue; MADS-box; MADS-like protein; CENTRORADIALIS;
KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
KW Inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein; ss.
OS
XX Lolium perenne.
XX
FN WO200233091-A1.
XX
PD 25-APR-2002.
XX
PE 17-OCT-2001; 2001MO-AU01311.
XX
PR 19-OCT-2000; 2000AU-0000873.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX (AGRE-) AGRERESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
DR WPI: 2002-452388/48.
XX
XX
PT New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases
XX
PS Claim 4; Fig 32; 290pp; English.
XX

The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in

CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles.
XX
SO Sequence 762 BP; 188 A; 178 C; 176 G; 220 T; 0 other;

Query Match 20.6%; Score 176; DB 24; Length 762;
Best Local Similarity 60.0%; Pred. No. 1,4e-31;
Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

OY 81 GACCTCTTATAGTACGAGACTTGTGAGACCTTCTGATCCCTTAATATGATCATC 140
DB 103 GAGCCTCTTATGTTGGTCGTCTCATTTGAGAACTTCGATCAACCCATGCTG 162
OY 141 ACTTAAAGTTACTTATGCGCAAGAGAGTGAC---TAAATGCTTGATCTAAGGCT 197
DB 163 AAGATGTAGCAACCTTATATCAACAAGCTGCTTCAATGATGATGATCTACCCA 222
OY 198 TCTCAGTTCAAAACCAAGCAAGTGTAGATGTGTGAGAGAACCTCAGAACTTCTAT 257
DB 223 TCAGCAGTTGATTAACCAAGAGTACAGGTTCAAGGGGGGACTTCGATCGATCTATTC 282
OY 258 ACTTGGTTATGTGATCCAGATGCTTCCAGTCTTACCAACCTCAGTCCGAGAAATAT 317
DB 283 ACATTTGTTATGCGGACCCAGATGCTCAGAGCAACATGATCCATCTGCGGAGCAT 342
OY 318 CTCATTTGTTGCTGACTGATTCCTCTACCACTGCAACAACCTTGGCATGAGATT 377
DB 343 CTTCACCTGATTTGATGATTAATATACCTGGACACAGATGCTTCAATTTGGGGGAGGTC 402
OY 378 GTGTGTACGAATAATCAAGTCCACCTGAGAAATTCATGCTGTATTAATATGTTT 437
DB 403 ATGACCTATGAGAGAGCCCAAGCCCAATTTGGAATCCACAGGTTATTTGTGCTTTC 462
OY 438 CGACAGCTTGGAGGCAAAAGTGTATGACAGGCTGCGCCACAACTTCAACCTGCG 497
DB 463 AAGCAGAAAGGAGCAACACTGATCTGCTTCTTCAAGGATCATTTCAACACCGCG 522
OY 498 GAGTTGCTGAGATCTACAAATCTCGCCTTCCCGCGCGCAGTTTCTACAAATGTCAG 557
DB 523 CAGTTTGTGTGATTAATGATCTTGGCTCCCTGTGGCTGCTTACTTCAATTTGTCAG 582
OY 558 AGGAGAGTGTGCTGCGGAGAGAAAGACTTAGATGCTT 597
DB 583 AGAGAGACTGCTGCCAGAGGCGCTGAAATGCAAGTCTT 622

RESULT 11
ABR82091
ID ABR82091 standard; cDNA: 792 BP.
AC ABR82091;
XX
DT 27-AUG-2002 (first entry)
XX
DE DNA encoding novel floral meristem identity protein *LpCENa*.
XX
KW Ryegrass; fescue; MADS-box; MADS-like protein; CENTRORADIALIS;
KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
KW Inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;

KM allergenic pollen; floral meristem identity protein; gene: ss.
 OS Lolium perenne.
 PN WO200233091-A1.
 XX 25-APR-2002.
 PD 17-OCT-2001; 2001WO-AU01311.
 PF 19-OCT-2000; 2000AU-0000873.
 PR 19-OCT-2000; 2000AU-0000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI WPI: 2002-452388/48.
 DR P-PSDB: ABG60933.
 XX
 DR New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APTALAZ, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX
 PS Claim 4: Fig 30; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APTALAZ (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box
 CC gene activities may alter flower, embryo and seed development, e.g.,
 CC enhance or inhibit embryo differentiation and growth or alter flower
 CC organ identity through conversion of one floral organ in another.
 CC Manipulation of CEN or HB activity in plants alters the control of phase
 CC change, flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles.
 XX
 XX Sequence 792 BP; 196 A; 181 C; 181 G; 232 T; 2 other;
 SQ
 Query Match 20.6%; Score 176; DB 24; Length 792;
 Best Local Similarity 60.0%; Pred. No. 1.4e-31;
 Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

DB 226 TCAGCAGTTGATCTAAACCAAGTAGAGTTACAGGGGGGTGACTTGGATCCTTATTC 285
 258 ACTTTGGTATGGTGATGCAGATGTTCCAAAGTCTAGCAACCCCTACCTCGAGAAATAT 317
 DB 286 ACATTGCTTATGGCGGAGCCAGATGTGCGGAGCCAAAGTATCGATTCGCGGAGCAT 345
 318 CTCGATTGGTTGGTGAAGTATATCCCTGCTACAACTGGAACAACCTTGGCAATGATAT 377
 DB 346 CTCGACTGATGTGATGATATATACCTGGGAGCAACAGATGCTTCATTTGGGGGAGTTC 405
 378 GTGTGTAGGAAATCCAAAGTCCGACTGCAGGAATTCATGCTGTCTTATATGTTT 437
 DB 406 ATGAGCTATGAGAGCCCAAGCCCAATGGAATCAACAGTTCAATTTTGTCTTTC 465
 438 CGACAGCTTGGCGAGCAACAGTGTATGACAGGCTGGCGCCAGCACTTCAACACTGCG 497
 DB 466 AAGCAGACGGAAGGAGGAGTATGATGCTGCTCTTCAAGGATATTTCAACACCCCG 525
 498 GAGTTTCTGAGATCTACATCTGCGCTCCGCGGCGGAGTTTCTACAAATGTCAG 557
 DB 526 CAGTTTGCTGTGATATGATGATGCTGCGCTCCGCTGCTGCTTACTTCAATGTCAG 585
 558 AGGAGAGTGTGCTGCGGAGGAGAGACCTTTAGATGCTT 597
 DB 586 AGAGAGACTGTGCTGCGAGAGGCGCTGMAAATGAGTTCT 625
 RESULT 12
 ABR82092
 ID ABR82092 standard; cDNA: 792 BP.
 XX ABR82092;
 AC 27-AUG-2002 (first entry)
 XX
 DE Novel floral meristem identity gene LpcEna contig #1.
 XX
 XX Ryegrass: fescue; MADS-box; MADS: MADS-like protein; CENTRORADIALIS;
 KW CEN: CEN-like protein; APTALAZ; AP2; AP2-like protein; HB;
 KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW hybrid seed production; flower organ identity; phase change; male sterility;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX
 OS Lolium perenne.
 PN WO200233091-A1.
 XX 25-APR-2002.
 PD 17-OCT-2001; 2001WO-AU01311.
 PF 17-OCT-2001; 2001WO-AU01311.
 PR 19-OCT-2000; 2000AU-0000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI WPI: 2002-452388/48.
 DR
 DR
 XX
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APTALAZ, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 PS Claim 4: Fig 32; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as

XX Sequence 1225 BP; 388 A; 249 C; 258 G; 330 T; 0 other;
SQ

Query Match	20.6%	Score 176; DB 34;	Length 1225;
Best Local Similarity	60.0%	Pred. No. 1.6e-31;	
Matches 312; Conservative	0;	Mismatches 205;	Indels 3; Gaps 1;

QY	81	GACCCTCTTTAGTAACCAAGTGTGGAGAGCTTCTATTCCTGTTATTAATGATCAATC	140
Db	153	GAGCCTCTATTGTGTGCTGTGCATTTGGAGAAAGTTCTGCATCTATTAAACCATGTGTC	212
QY	141	ACTCTAAAGCTTACTATATGCCAAAGAGAGTGAC--TATGGCTTGATCTPAAGGCTT	197
Db	213	AAGATGTACCAACCTTAACTCAAAACACCTGTCTTCATAGTATGATAGCTCTACCCA	272
QY	198	TCTCAGTTGTAACCAACGACAGCTTGATTTGGTGGAGAAACCCCTAGAAACTCTAT	257
Db	273	TCAGCACTTTGATCTTAACCAACAGTATGAGAGTTCTAGGGGGGTAGCTTGCCATCTTATTC	332
QY	258	ACATTGGTATATGTGATATCCAGATGTGTTCCAAAGTCCTAGCAACCCCTCACTCCAGATAAT	317
Db	333	ACATTGGTATATGGGGGACCCAGATGTGCCAGCAACAGTATCCGATCTTGGCGGAGCAT	392
QY	318	CTCATTTGGTGTGGAGACTGATATCCCGCTGACACAACTGGAAACACTTTGGCAATGAGATT	377
Db	393	CTTCTACTGGAATGTCACTAATATATACCTGGGCAACACAGATCTTCATTTGGGGGGAGGTC	452
QY	378	GTTGTTACGAAATCCCAAGTCCCACTGACAGGAATTCATGTTGCTGTTATATATGTTT	437
Db	453	ATGAGCTATAGAGACCCCAAGCCCAACATTGGAAATCCACAGTTTCAATTTTGTGTCTTTC	512
QY	438	CGACAGCTTGGCAGGCCAAAGATGTATGACCAACAGGGTGGCGGCCAGAACTTCAACACTCGC	497
Db	513	AAGCAGAGCGAAGGACGACTGTATCTGTGCTCTCTCTCAGGCACTCTTTCACACACCCGC	572
QY	498	GAGTTTGCTGAGATCTTCAACTCTCGGCTTCCCGTGGCCGACAGTTTCTTCAATTTGTCA	557
Db	573	CAGTTTCTGTGATATATGATCTTGGCCCTCCCTGTGGCTCTCTGTTACTTCAATTTGCAG	632
QY	558	AGGAGAGTGGCTGCGGAGGAAGAAGACTTTAATAGCTT	597
Db	633	AGAGAGCTCTGCCAGAGAGCCCTGAAAATTCAGATTTCT	672

RESULT 14
ABK82094
ID ABK82094 standard; cDNA; 787 BP

AC	ABK82094;
XX	
DT	27-AUG-2002 (first entry)

Novel floral meristem identity gene *LpCENa* contig #3.

KW
KX
KY
KZ
LA
LB
LC
LD
LE
LF
LG
LH
LI
LJ
LK
LL
LM
LN
LO
LP
LQ
LR
LS
LT
LU
LV
LW
LX
LY
LZ
MA
MB
MC
MD
ME
MF
MG
MH
MI
MJ
MK
ML
MM
MN
MO
MP
MQ
MR
MS
MT
MU
MV
MW
MX
MY
MZ
NA
NB
NC
ND
NE
NF
NG
NH
NI
NJ
NK
NL
NM
NN
NO
NP
NQ
NR
NS
NT
NU
NV
NW
NX
NY
NZ
OA
OB
OC
OD
OE
OF
OG
OH
OI
OJ
OK
OL
OM
ON
OO
OP
OQ
OR
OS
OT
OU
OV
OW
OX
OY
OZ
PA
PB
PC
PD
PE
PF
PG
PH
PI
PJ
PK
PL
PM
PN
PO
PP
PQ
PR
PS
PT
PU
PV
PW
PX
PY
PZ
QA
QB
QC
QD
QE
QF
QG
QH
QI
QJ
QK
QL
QM
QN
QO
QP
QQ
QR
QS
QT
QU
QV
QW
QX
QY
QZ
RA
RB
RC
RD
RE
RF
RG
RH
RI
RJ
RK
RL
RM
RN
RO
RP
RQ
RR
RS
RT
RU
RV
RW
RX
RY
RZ
SA
SB
SC
SD
SE
SF
SG
SH
SI
SJ
SK
SL
SM
SN
SO
SP
SQ
SR
SS
ST
SU
SV
SW
SX
SY
SZ
TA
TB
TC
TD
TE
TF
TG
TH
TI
TJ
TK
TL
TM
TN
TO
TP
TQ
TR
TS
TT
TU
TV
TW
TX
TY
TZ
UA
UB
UC
UD
UE
UF
UG
UH
UI
UJ
UK
UL
UM
UN
UO
UP
UQ
UR
US
UT
UU
UV
UW
UX
UY
UZ
VA
VB
VC
VD
VE
VF
VG
VH
VI
VJ
VK
VL
VM
VN
VO
VP
VQ
VR
VS
VT
VU
VV
VW
VX
VY
VZ
WA
WB
WC
WD
WE
WF
WG
WH
WI
WJ
WK
WL
WM
WN
WO
WP
WQ
WR
WS
WT
WU
WV
WW
WX
WY
WZ
XA
XB
XC
XD
XE
XF
XG
XH
XI
XJ
XK
XL
XM
XN
XO
XP
XQ
XR
XS
XT
XU
XV
XW
XX
XY
XZ
YA
YB
YC
YD
YE
YF
YG
YH
YI
YJ
YK
YL
YM
YN
YO
YP
YQ
YR
YS
YT
YU
YV
YW
YX
YY
YZ
ZA
ZB
ZC
ZD
ZE
ZF
ZG
ZH
ZI
ZJ
ZK
ZL
ZM
ZN
ZO
ZP
ZQ
ZR
ZS
ZT
ZU
ZV
ZW
ZX
ZY
ZZ

OS Lolium perenne.

PN WO200233091-A1

PD 25-APR-2002.

17-OCT-2001; 2001WO-AU01311.

PR 19-OCT-2000; 2000AU-0000873.

PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
XX WPI; 2002-452388/48.

PT New substantially purified or isolated polypeptide e.g., MADS-box, CENTRORHINALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or fescue species, useful for controlling plant life cycles and/or growth phases -

PS Claim 3; Fig 32; 290pp; English.

CC The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such a
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-1-LIKE
CC proteins, APTERATA2 (AP2) and AP2-LIKE proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants
CC. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box
CC gene activities may alter flower, embryo and seed development, e.g.,
CC enhance or inhibit embryo differentiation and growth or alter flower
CC organ identity through conversion of one floral organ in another.
CC Manipulation of CEN or HB activity in plants alters the control of phases
CC change, flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced biomass in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles.

Sequence 787 BP; 194 A; 180 C; 179 G; 228 T; 6 other;

Query Match	20.4%	Score 175;	DB 31;	Length 787;
Best Local Similarity	59.8%	Pred. No. 2.4e-31;		
Matches 311; Conservative	0;	Mismatches 206;	Indels 3;	Gaps 1;

QY	81	GACCTCTTATAGTAACACAGTGTGGAGACCTCTGATCCGTTAATATAGATCAATC	140
Db	106	GAGCTCTTATGTGGTCGTGATTTGGAGAAATCTTCATTCATTAAACCCATGTGTG	165
QY	141	ACITTAAGGTTACTTATATGGCCAAAGAGAGGTGAC---TATGGCTTGATCTAAAGGCT	197
Db	166	AAGATGTAGCAACCTTAATCTCAACAAGCTGTCTTCAATGCTATAGCTTACC	222
QY	198	TCCTCAGTTCAAAACCAAGCCACAGGTTGACATTTGTGGAGACACCTCAGCAACTTCTAT	255
Db	226	TCACACATTTGATATCTAAACCAAGGTTAGAGGTTTCAGGGGGGTGACTTCGCATCCTTTATTC	285
QY	258	ACTTGGTTATGGGATGCCAGATGTCCAAAGTCTGACCAACCTCCACCTCCGGAAAT	317
Db	286	ACATTTGTTATGGGGGACCCAGATGTCCACGAGACCAAGTGATCTCGTATTCGGCGGACAT	345
QY	318	CTCCATTGGTGTGGACATGATATCCCTGCTACAACTGGAACACCTTTGGCAATGAGATT	377
Db	346	CTTCACATCGAATGTCACTAATATATACCTCGGGGCAACACATGCTTCATTTTGGGGGGGAGATC	405
QY	378	GTCGTATACGAAAATCCCAAGTCCCATTCGACAGGAATTCATCGTGTGCTGTTTATATATGCTTT	437

Db 406 ATGAGTATGAGACCCCAACCAATTCAGATTCATTTTGTGCTTC 465
QY 438 CGAAGCTTGGCAGCAACAGTGTATGCACAGGTGGCCCAACTTAACTGCG 497
Db 466 AAGGANAAGCGAAGGACGATCTGTGCTTCCTTCAGAGATCATTTCAACCCGCG 525
QY 498 GAGTTGCTGAGATCTCAATCTCGGCTTCGCCGTGCGGAGTTTCTACAAATGTCAG 557
Db 526 CAGTTGCTGTGATTAATGATCTTGCCCTCCCTGTGCTGCTGTACTTCAATTTGTCAG 585
QY 558 AGGAGAGTGGCTGCGGAGGAAGACTTTAGATGCTT 597
Db 586 AGAGAGCTGCTGCCAGAGGCGCTGAAATCAGATCTT 625

RESULT 15
AAC90668
ID AAC90668 standard; cDNA; 519 BP.
XX
AC AAC90668;
XX
DT 20-MAR-2001 (first entry)
XX
DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
XX
KW Strawberry; flowering regulation; floral homeotic gene; field crop;
XX
KW harvesting; fruit production; ss.
XX
OS Fragaria vesca.
XX
SN WO200071722-A1.
XX
PD 30-NOV-2000.
XX
PE 24-MAY-2000; 2000MO-US14297.
XX
PR 25-MAY-1999; 99US-0318789.
XX
PR 24-MAY-2000; 2000US-0318789.
XX
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
XX
PI Oeller P, Guttererson N;
XX
DR WPI: 2001-025165/03.
XX
DR P-PSDB: AAB50271.
XX
PT Novel nucleic acid involved in controlling plant flowering processes is
PT useful for generating transgenic plants, in particular strawberry
PT plants having altered flowering behavior such as early, delayed or
PT day-neutral flowering
XX
XX
PS Claim 23; Page 94-95; 97pp; English.
XX
CC The present invention provides the nucleic acid and protein sequences of
CC a number of proteins from the strawberry which are involved in the
CC regulation of flowering. These were identified using primers based on the
CC homologous sequences from A. thaliana, B. napus and R. sativus. They can
CC be used in the production of transgenic field crops whose flowering is
CC regulated and the time of fruiting and harvesting can be manipulated.
XX
SQ Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;

Query Match 18.8%; Score 161.2; DB 22; Length 519;
Best Local Similarity 57.9%; Pred. No. 3.6e-28;
Matches 286; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 71 AATATTAAGAGACCTCTTATAGTAAGAGAGTGTGAGAGCTTCTTGATCCGTTAA 130
Db 6 AAGATGTCGAGACCTCTAGCTGTGGAAGATGATAGAGATGTTCTTGATCCCTCAC 65
QY 131 TAGATCAATCACTCTAAGGTTACTTATGCGCAAGAGAGTGAATAATGCTTGATCT 190
Db 66 CCCACATCAAAATGATGTCTCTTACACAGACGAGCTGCTGCAATGACATGAGACT 125

QY 191 AAGGCTTCTGAGTTCAAAAAGCCAAAGATTGAGATTGTTGAGAGAAGACCTCAGAA 250
Db 126 CTTCCTTCTGACGACACCGCCAAACCTAGATGATTAAGAGGCGACATGATC 185
QY 251 CTTCATATCTTGGTTATGATGATCGAATGTTCCAGTCTAGCAACCCCTCAGCTCG 310
Db 186 ATTCTTACTCTGTAATGACAGACCCAGATGTCTGCGCTATGATCTTATTGAA 245
QY 311 AGAATATCTCATTTGTTGTTGATGATATCTCTGCTACAACTGGAACACCTTTGCAA 370
Db 246 AGAGACCTGCACATGATGATGACAGACATTCCTGCGACACAGATCTACATTTGGAAG 305
QY 371 TGAGATTGTGTAGCAAAATCCAAAGTCCCACTGCAAGAAATCATCTGCTGCTTAT 430
Db 306 AGAAGTGTGAGCTACGAGATGCCAAAGCCAAACATAGGCATCCACAGGTTGTGTTGT 365
QY 431 ATTTGTTGACAGCTTGGCAGGCAACAGTGTATGCACAGGTTGGCCGACAACTTCAA 490
Db 366 TCTCTTCAATGCAAAAAGCAAGCACTGCTGACCCGCTTCTCAAGGATCACTTCAA 425
QY 491 CACTGCGAGTTTGTGATCTACATCTGCGCTTCCCGTGGCCGACGTTTCTACAA 550
Db 426 CACCGAACCTTCCGAGCCGAAACGACCTTGTGTTCTGTTGCTGCCGTTTACTTCAA 485
QY 551 TTGTACAGAGGAGA 564
Db 486 TGCACAGAGAGAAA 499

Search completed: May 2, 2003, 10:45:30
Job time : 289.5 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 05:54:34 ; Search time 1783.5 Seconds
(without alignments)
7773.107 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856

Sequence: 1 tctgaactagtgatccccc.....aaaaaaaaaactctcgag 856

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estcmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516.4	60.3	518	10	AV563203
2	494	57.7	494	10	AV563277
3	423	49.4	423	10	AV788551
4	234	27.3	551	10	BE590867
5	231.6	27.1	659	14	BQ797327
6	206	24.1	206	10	AV560420

7	199.4	23.3	1168	11	AV11549	AV11549	Zea mays
8	198.4	23.2	505	10	BE498304	BE498304	WHE0963_B
9	196.8	23.0	491	12	BF483056	BF483056	WHE2314_C
10	184.6	21.6	542	10	AV937451	AV937451	AV937451
11	181	21.1	781	12	BE647258	BE647258	EST50867
12	173.2	20.2	718	13	BM407295	BM407295	EST581622
13	166.8	19.5	498	13	BJ453783	BJ453783	BJ453783
14	164	19.2	671	13	BJ448552	BJ448552	BJ448552
15	157.2	18.4	597	13	BJ315664	BJ315664	BJ315664
16	154.6	18.1	476	14	BJ018869	BJ018869	BJ018869
17	152.4	17.8	572	13	BJ461322	BJ461322	BJ461322
18	152.4	17.8	574	13	BJ456274	BJ456274	BJ456274
19	151.2	17.7	528	14	BM814255	BM814255	EST592348
20	150.8	17.6	395	17	BE580799	BE580799	BOGFM69TF
21	146.8	17.1	520	10	BE602964	BE602964	BE602964
22	143	16.7	574	12	BF259482	BF259482	HVSMH010
23	142.2	16.6	773	17	BH542868	BH542868	HVSMH001
24	141	16.6	459	9	AL385107	AL385107	MCBC26D07
25	140.8	16.5	432	10	BE319228	BE319228	NF015E08R
26	139.4	16.4	580	13	BI478762	BI478762	949070A05
27	139	16.2	456	10	AM684982	AM684982	NF023H07N
28	136.8	16.0	545	13	BJ212200	BJ212200	BJ212200
29	132.6	15.5	383	10	AM927655	AM927655	945014B02
30	131.2	15.3	478	10	AM684071	AM684071	NF011G04N
31	127.6	14.9	543	10	AM284098	AM284098	LGI_267_G
32	127.2	14.9	558	13	BI426705	BI426705	sag07c12
33	122.6	14.3	381	14	T44654	T44654	7917_Lambda
34	122.6	14.3	687	13	BI679012	BI679012	SWS105_S
35	116.2	13.6	463	10	AW707147	AW707147	sk10C07_Y
36	115.6	13.5	337	13	BI751372	BI751372	Ta01_16H0
37	114.2	13.3	417	12	BF473137	BF473137	WHE0922_A
38	113.8	13.3	357	13	BI941606	BI941606	sc77901_Y
39	113.2	13.2	682	13	BI311589	BI311589	EST531333
40	105	12.3	333	10	BE500873	BE500873	WHE0991-F0
41	103.2	12.1	608	12	BC463850	BC463850	EMI_51_F0
42	102.8	12.0	586	13	BM269830	BM269830	sak20H06
43	101.6	11.9	341	13	BI750810	BI750810	Ta01_02c1
44	101.4	11.8	522	10	AM981994	AM981994	PC22E11_P
45	101.4	11.8	627	17	AQ289409	AQ289409	nbxd0035E

ALIGNMENTS

RESULT 1
LOCUS AV563203 518 bp mRNA linear EST 07-SEP-2000
DEFINITION AV563203 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ183b01F 3', mRNA sequence.

ACCESSION AV563203
VERSION AV563203.1 GI:8734629
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana
thale cress.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries

JOURNAL
MEDLINE
COMMENT

CONTACT: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizukazusa.or.jp URL: http://www.kazusa.or.jp/en/plant/.
1. 518
/organism="Arabidopsis thaliana"
/strain="Columbia"

```

/db_xref="taxon:3702"
/clone_1b="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      163 a      120 c      85 g      150 t
ORIGIN

```

Query Match	60.3%	Score 516.4	DB 10	Length 518
Best Local Similarity	99.8%	Pred. No. 1.9e-79		
Matches 517; Conservative	0	Mismatches 1	Indels 0	Gaps 0

[illegible]

RESULT 2	AV562377/c	LOCUS	AV562377	494 bp	mRNA	linear	EST 07-SEP-2000
DEFINITION	AV562377	Arabidopsis thaliana green siliques Columbia	thaliana cDNA clone SQ169B07F 3', mRNA sequence.				Arabidopsis

VERSION	AV562377.1	GI:8733803
KEYWORDS	EST.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 494)	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.	A large scale analysis of cDNA in Arabidopsis thaliana: Generation

JOURNAL DNA Res. 7, 175-180 (2000)

COMMENT

The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

FEATURES
source location/Qualifiers
1. .494

```

/r/tissue_type="green_siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

```

Query Match	57.7%	Score 494	DB 10	Length 494
Best Local Similarity	100.0%	Pred. No. 1,4e-75		
Matches 494	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 335	TGATTCCTCGTACAACTGAAACAACCTTTGGCAATGAGATTGTGTGTACGAAATTC	394		
Db				
494	TGATATCCCTGTAACACTGGAAACACCTTTGGCAATGAGATTGTGTGTACGAAATTC	435		
QY 395	AAGTCCCACTGAGAGAAATTCATCGTGTGTTATTTATTTGTTTCAGACACTTGGCAGGCA	454		
Db	434	AAGTCCCACTGAGAGAAATTCATCGTGTGTTATTTATTTGTTTCAGACACTTGGCAGGCA	375	
QY 455	AACACTGTATGACACAGGGTGGCGCCAGAACCTTCAACACTCGCGAGTTTGCTGACATCTA	514		
Db	374	AACACTGTATGACACAGGGTGGCGCCAGAACCTTCAACACTCGCGAGTTTGCTGACATCTA	315	
QY 515	CAATCTCGGCGCTCCCGTGGCGCAGTTTTCACAATGTGTCAGAGGAGAGTGGTCGGG	574		
Db	314	CAATCTCGGCGCTCCCGTGGCGCAGTTTTCACAATGTGTCAGAGGAGAGTGGTCGGG	255	
QY 575	AGGAAGAAGACTTTAGATGGCTTCTCCCTTTATAACAATGATATTTGTCATCTGTGATG	634		
Db	254	AGGAAGAAGACTTTAGATGGCTTCTCCCTTTATAACAATGATATTTGTCATCTGTGATG	195	
QY 635	AGATTATAGCATCTATACTATTTTAAATTAACCATTTTATGATACGAGTAACGAACG	694		
Db	194	AGATTATAGCATCTATACTATTTTAAATTAACCATTTTATGATACGAGTAACGAACG	135	
QY 695	GTGATGATGCGCTATAGTAGTGTCAATATATTAAGTGTATATAAATGAGAGGGGAGGAA	754		
Db	134	GTGATGATGCGCTATAGTAGTGTCAATATATTAAGTGTATATAAATGAGAGGGGAGGAA	75	
QY 755	AATGAGAGTGTTTTACTTATATAGTGTGTGATGCGATATATATTAATCTACATGAAT	814		
Db	74	AATGAGAGTGTTTTACTTATATAGTGTGTGATGCGATATATATTAATCTACATGAAT	15	
QY 815	GAAGCTATATTT 828			
Db	14	GAAGCTATATTT 1		

RESULT	3	423 bp	mrna	linear	EST 28-MAR-2002
LOCUS	AV788551/c				
DEFINITION	AV788551				
	AV788551	Arabidopsis thaliana	CDNA clone	RAFL06-80-B19 3'	

KEYWORDS EST: thale cress.
SOURCE Arabidopsis thaliana
ORGANISM

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCES

Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.

TITLE and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rcc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source
Location/Qualifiers
1. 423
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF106-80-B19"
/clone_lib="RAF16"
/dev_stage="plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
/note="Site: 1: SstI; site: 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT 131 a 99 c 70 g 123 t
ORIGIN

Query Match 49.4%; Score 423; DB 10; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

382 GTTACGAAATCCAAAGTCCACGACGAGAAATCATCGTGTGTTATATGTTTCGAC 441
|||||
423 GTTACGAAATCCAAAGTCCACGACGAGAAATCATCGTGTGTTATATGTTTCGAC 364
|||||
442 AGCTGGCAGCAAAAGTATGACACGAGGTCGCGCAACTTCAACACTCGCGAGT 501
|||||
363 AGCTGGCAGCAAAAGTATGACACGAGGTCGCGCAACTTCAACACTCGCGAGT 304
|||||
502 TTGCTGAGATCTACATCTCGGCTTCCGTCGCGCAGTCTTCAATTTGTCAGAGG 561
|||||
303 TTGCTGAGATCTACATCTCGGCTTCCGTCGCGCAGTCTTCAATTTGTCAGAGG 244
|||||
562 AGAGTGGCTCGGAGCAAGACTTTAGATGGCTTCTCCTTTATTAACCAATGATATT 621
|||||
243 AGAGTGGCTCGGAGCAAGACTTTAGATGGCTTCTCCTTTATTAACCAATGATATT 184
|||||
622 GCATACCTGATGATATTTGATGATCTATGATATTTAATTAATTAACCAATTTATGATA 681
|||||
183 GCATACCTGATGATATTTGATGATCTATGATATTTAATTAATTAACCAATTTATGATA 124
|||||
682 CGAGTAAAGCAAGCGTATGATGCTATAGTATGTTCAATATATAGTGTATATAAATG 741
|||||
123 CGAGTAAAGCAAGCGTATGATGCTATAGTATGTTCAATATATAGTGTATATAAATG 64
|||||
742 AGAGGGGGAGGAAATGAGAGTGTCTTACTTATATAGTGTGTGATGGGATATATATTA 801
|||||
63 AGAGGGGGAGGAAATGAGAGTGTCTTACTTATATAGTGTGTGATGGGATATATATTA 4
|||||
802 ATC 804
|||
3 ATC 1
Db

RESULT 4
BE590867 551 bp mRNA linear EST 18-AUG-2000
LOCUS BE590867
DEFINITION WHE0855_C01_E0125 wheat 20-45 DAP spike cDNA library Triticum
aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
ACCESSION BE590867

VERSION BE590867.1 GI:9845940
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Izzo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
Unpublished (2000)

TITLE
JOURNAL
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: StrataGene SR primer.

FEATURES

source
Location/Qualifiers
1. 551
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0855_C01_E01"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spoke and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; site: 1: EcoRI; site: 2: XhoI; plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)"
BASE COUNT 106 a 171 c 168 g 106 t
ORIGIN

Query Match 27.3%; Score 234; DB 10; Length 551;
Best Local Similarity 68.9%; Pred. No. 6.2e-31;
Matches 321; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

78 AGAGACCCCTCTTATAGTACGAGAGTGTGGAGACGTTCTTGATCCGTTTAATGATCA 137
|||||
85 AGAGACCCGCTGTGTGGAGGTTGTGGGAGCAGCGTGGACCCCTTCATCCGAGCC 144
|||||
138 ATCACTCTAAAGTTACTTATGAGCCAAAGAGAGGATGATGGCTTGATCTAAGGCT 197
|||||
145 ACCAAGCTCAGGAGTACCTTGGGACAGACCGGTGTCACAGCGCTGGAGCTAAGCG 204
|||||
198 TCTCAGGTTCAAAACAGCCAAAGTTGAGATGTTGGAGAGAGCTCAGGAACCTCTAT 257
|||||
205 TCCATGGTCCGCCAGACAGCCAGAGGTTGAGGTGGCGGCAATGAGATGAGAGCTTCTAC 264
|||||
258 ACTTGGTATGATGATCCAGATGTTTCAAGTCTTCAACACCTCAGCTCCGGAATAT 317
|||||
265 ACACCTGATGATGATGATCCAGATGCTCAAGTCTCAACGCTTCAAGCTTATGAGAGTAT 324
|||||
318 CTCATGTTGTTGATGATATCCCTGCTCACTGGAACACCTTGGCATGAGATTT 377
|||||
325 CTCACATGGCTTGTGACAGATATCCCGGTACCACTGTGATCTTCCGGCAGAGAGTG 384
|||||
378 GTGTGTACGAAATCCAAAGTCCACATGACGAATTCATCGTGTCTTATATTTGTTT 437
|||||

Db 385 ATGTCTACGAGAGCCCTGTCGCCAGCATGGGATCATCTGCTGCTGCTTC 444
QY 438 CGACAGCTTGGACCAACAGATGTATGCACAGAGGTGGCGCCAGACTTCAACACTGC 497
Db 445 CAGCAGCTGGCGCCGACACCGTGTACGCTCCCGGTGGCGCCAGAACTTCAACACGAG 504
QY 498 GAGTTTGGTGAATCTACATCTGGCCCTTCCCGTGGCCGAGTTT 543
Db 505 GACTTCGCCGAGCTCTACACCTCGGCCCTGTCGCCGCTCT 550

RESULT 5
BQ797327/c 659 bp mRNA linear EST 30-JUL-2002
LOCUS BQ797327
DEFINITION EST 6265 Ripening Grape berries Lambda zap II library Vitis
vitisfiera cDNA clone RT071D11 3', mRNA sequence.
ACCESSION BQ797327
VERSION BQ797327.1 GI:22012293
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 659)
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
CONTACT: Romieu C.
JOURNAL Institut National de la Recherche Agronomique
COMMENT 2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..659
/organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="RT071D11"
/clone_lib="Ripening Grape berries Lambda zap II Library"
/dev_stage="ripening stage"
/note="Organ: Fruit; Vector: Lambda zap II; Site_1: Eco RI
; Site_2: XhoI; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier,N.,
Ageorges,A., Abbal,P., Romieu,C. In J. Plant Physiol. 158
(12): 1575-83 2001"

BASE COUNT 197 a 155 c 124 g 183 t
ORIGIN

Query Match 27.1%; Score 231.6; DB 14; Length 659;
Best Local Similarity 74.6%; Pred. No. 1.5e-30;
Matches 291; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Db 479 GTTATATAGAGCCACCACCCAGCTGGAGTTTCATGCTTTGTTATGTTTCG 420
QY 440 ACAGCTGGACGCAACAGTATGACACCGGGGGCCGAGACTTCAACACTCGGGA 499
Db 419 CCAACTGGTAGGACAGATGTATGACACGAGGGGGCCAAATTTCAACACTAGGGA 360
QY 500 GTTTCCTAGATCTCAATCTCGCCCTCCGCGCCGAGTTTCTCAATTTGTACAG 559
Db 359 CTTTCTAGCTTTATATCTGTTGCTTCTGCTGCTGTTTAACTGCCAAG 300

QY 560 GGAGAGTGGCTGCGGAGACAGACTTTA 589
Db 299 GGAGGCGGCTGCGGCTGTCGAGATCATTA 270

RESULT 6
AV560420/c 206 bp mRNA linear EST 07-SEP-2000
LOCUS AV560420
DEFINITION AV560420 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ134D05F 3', mRNA sequence.
ACCESSION AV560420
VERSION AV560420.1 GI:8731846
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 206)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
COMMENT 20363093
CONTACT: Erika Asamizu
JOURNAL The First Laboratory for Plant Gene Research
COMMENT Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source Location/Qualifiers
1..206
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ134D05F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 69 a 43 c 28 g 66 t
ORIGIN

Query Match 24.1%; Score 206; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-26;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible][illegible]


```

/db_xref="taxon:77009"
/clone="bahl1n08"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
120 a 150 c 146 g 124 t 2 others
BASE COUNT
ORIGIN

```

```

RESULT 12
BM407295          718 bp  mRNA  linear  EST 22-JAN-2002
LOCUS             EST581622 potato roots Solanum tuberosum cDNA clone cPRO30M16 5'
DEFINITION        end, mRNA sequence.
ACCESSION         BM407295
VERSION           BM407295.1  GI:18258925
KEYWORDS          EST.
SOURCE            potato.
ORGANISM          Solanum tuberosum
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE         van der Hoeven,R., Sun,H., Karanycheva,S.A., Tsai,J., Van Aken,S.,
                  Uteback,T., Chelimgo,A., Bougrl,O., Buell,C.R., Ronning,C.,
                  Tanksley,S. and Baker,B.
AUTHORS           Generation of ESTs from potato roots
                  Unpublished (2001)
JOURNAL           Contact: Research Genetics, Libraries Division
                  Tel: 1-800-711-6195
                  Email: cdna@resgen.com
COMMENT           For clone info: please contact Research Genetics, Libraries
                  Division tel 1-800-711-6195, email cdna@resgen.com
                  Seq primer: T3.
FEATURES
    source         location/Qualifiers
    1..718
    /organism="Solanum tuberosum"
    /cultivar="Kennebec"
    /db_xref="taxon:4113"
    /clone="cPRO30M16"
    /clone_lib="potato roots"
    /tissue_type="roots"
    /dev_stage="in vitro grown stem cuttings"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
    XhoI; supplier: Cornell University, Tanksley lab;
    sequencing: The Institute for Genomic Research. Roots were
    isolated from in vitro grown stem cuttings on CM medium.
    Roots were isolated two weeks after plugging the stem
    cuttings from in vitro grown plants on medium."
BASE COUNT        243 a 128 c 142 g 205 t
ORIGIN
Query Match      20.2%; Score 173.2; DB 13; Length 718;
Best Local Similarity 60.2%; Pred. No. 1.5e-20;
Matches 324; Conservative 0; Mismatches 208; Indels 6; Gaps 2;
QY 53 AAGATCAAGATGCTATATAATATAGAGACCCCTTATAGTAAAGAGAGTTGTGAGA 112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 AAGATCAATATGCTCTGTAGAGATATGAAACCACTTATGTCAGAGATGATGAGA 87
QY 113 CGTTCTTGATCCGTTTAAATAGATCAATCACTTAAAGGTTA---CTTATGCCAAAGAGA 169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 AGTAGTTGATAGTTTCAATCCAGTGTAAGAAATGAAATGATATATATATGGAAGCAACA 147
QY 170 GGTGACTAATGCTTGATCTAAGGCTTCTCAGGTTCAAAACAGCCAGAGATTGAGAT 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 AGTGTTATGCTGACGAACTCATGCCCTCATTCATTCCTTAAAGCCTCGTGAGGAT 207
QY 230 TGGTGAAGAACCTCAGGAACCTTATCTTATGTTTGGTTATGTTGATCCAGATGTTCCAAG 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 TGGTGAAGAACATAGATCTGCTTATACATCATCATGATCATGATCCAGATGTTCCAAG 267
QY 290 TCCTAGCAACCTCACCCTCGAGATATATCCATTGTTGGTATGATGATATCCCTGTAC 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 TCCTATGATCTTACTTAAAGGAACAACCTCCACTGATGTTGATGATATTTCTGTTTC 327
QY 350 AACTGGAACAACCTTTGGCAATGAGATGTGTGTTACGAAATCCAAAGTCCCACTGACAG 409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 AACTGATGCTTCTTTGGAAAAGAGATGAGACTACGATAGTCCAAACCACTGATCGG 387

```

```

QY 410 AATTCATCGTCGTGTTTATATATGTTTCGACAGCTT---GGCAGGCCAAACAGTGTATGC 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 GATTCATCGATACGTGTTCTGATATATATAGCAAAATATAGAGAAACAAACAGTGAATC 447
QY 467 ACCAGGGTGGGCCAGAACTTCAACACTCGCGAATTTTGCTGATCTACATCTCGGCT 526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 ACCAGTAACAAGATATATTTCAACACTCAAAAATTTTCACACAGCAAAAATGATGGCTTC 507
QY 527 TCCGTGGCCGACGTTTCTTACATTTGTCAGAGGAGAGTGGTGGGAGAGAGA 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 CCCGTGTCCTCTCTACTTATATGCCCCAAAGAAACCTCTCTGAGAAAGATGA 565
RESULT 13
BJ453783          498 bp  mRNA  linear  EST 23-MAY-2002
LOCUS             BJ453783 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION        vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
                  baak44h08 5', mRNA sequence.
ACCESSION         BJ453783.1  GI:21132359
VERSION           BJ453783
KEYWORDS          EST.
SOURCE            Hordeum vulgare subsp. vulgare.
ORGANISM          Hordeum vulgare subsp. vulgare
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
                  ; Triticeae; Hordeum.
                  1 (bases 1 to 498)
REFERENCE         Sato,K., Saisho,D. and Takeda,K.
                  barley EST sequencing project in NIG and Okayama Univ
                  Unpublished (2002)
JOURNAL           Contact: Tadasu Shin-I
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshin@genes.nig.ac.jp.
FEATURES
    source         location/Qualifiers
    1..498
    /organism="Hordeum vulgare subsp. vulgare"
    /cultivar="Akashinriki"
    /db_xref="taxon:112509"
    /clone="baak44h08"
    /clone_lib="K. Sato unpublished cDNA library, cv.
    Akashinriki vegetative stage leaves"
    /tissue_type="leaves"
    /dev_stage="vegetative stage"
BASE COUNT        132 a 114 c 129 g 123 t
ORIGIN
Query Match      19.5%; Score 166.8; DB 13; Length 498;
Best Local Similarity 60.6%; Pred. No. 2.3e-19;
Matches 292; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
QY 102 GTTGTTGAGAGCTTCTGATCCGTTTATATAGATCAATCACTTAAAGTTACTTATGCG 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 18 GTTATGCAMAGATGTGTTGATTCATTCATTCATCAACCGTTCAATTAAGATAGCTTCAAC 77
QY 162 CAAGAGAGGTACTATAGCTTGATCTGATCTTAAGGCTTCTCAGTTCAAAACAGCCAAAG 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 AATAGGCTAATGCTTGGCAGGCTGCTGAGACTAAGCACTTCGCAATTTGATAGTAAAGCCACGA 137
QY 222 GTTGAGATTGGAGAGAGACCTCAGAACTTCTATATCTTGTGTTATGGTATCCAGAT 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 GTTGATTGCGTGGCAGTAGATGATAGAGTTCTACACACCTGATATTTGGTGAATCCAGAC 197
QY 282 GTTCAAGTCTTCAACAACCTCAGCTCCGAGAAATATCTCCATGTTGTGATGATATC 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 GCTCAAGGCCCAAGTACCACCATCATCAAGGAGTACTTGCATGATGATGATGATGACATC 257
QY 342 CCTGCTACAACTGGAACAACCTTTGGCAATGATGATGTGTGTACGAAATCCAAATGCC 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 258 CTTGGAACAACGTGTCAGCTTCGCCGAGAGCTTGAATTGANAAGACAGAACCA 317

Qy 402 ACTGACGAGATTCATCGTGTGCTTTATATATTTTGACAGCTTGGACGCAACAGATG 461

Db 318 AGATCTGTATTCACCGAGATGATTTGTGCTTCCAGCAACATGAGGAGGATACACTT 377

Qy 462 TATGACACAGAGGTGGCCGACAGACTTCACACCTCGCGATTTGCTGAGATATCAATATC 521

Db 378 TTTCACACAGACGTCGCCAGCAAACTTCAGCTGCAGAGAACTTGTACGACATACACTTA 437

Qy 522 GGCCTTCCTGCGCCGAGTTTCTACAAATTTGAGAGGAGAGTGGCTGGGAGAGAA 581

Db 438 AACGT---GTGCTGCTCATATTTCAACTGTCAAGGAGAGGTGATTCAGCGGAGAA 494

Qy 582 AG 583

Db 495 AG 496

RESULT 14

BJ448552

LOCUS BJ448552 671 bp mRNA linear EST 23-MAY-2002

DEFINITION BJ448552 K. Sato unpublished cDNA library, cv. Akashinriki

vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

bakx20f16 5', mRNA sequence.

ACCESSION BJ448552

VERSION BJ448552

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare.

ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE 1 (bases 1 to 671)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

FEATURES

Location/Qualifiers

1..671

source

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Akashinriki"

/db_xref="taxon:112509"

/clone="bakx20f16"

/clone_id="K. Sato unpublished cDNA library, cv.

Akashinriki vegetative stage leaves"

/tissue_type="leaves"

/dev_stage="vegetative stage"

BASE COUNT 189 a 142 c 166 g 173 t 1 others

ORIGIN

Query Match 19.2%: Score 164; DB 13; Length 671;

Best Local Similarity 60.5%: Pred. No. 6e-19;

Matches 288; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

Qy 112 ACCTTTCGATCCGTTTATATGATCAATCACTTAAGGTTACTTATGGCCCAAGAGAGG 171

Db 29 ATGTGCTTGATCATTTACATCAACCGTTCCATTAGCATAGCCTACACAATAGGCTAG 88

Qy 172 TGACATAAGGCTTGATCAAGCGCTTCTCAGTTTCAAAACAGGCAAGAGTGGAGATTG 231

Db 89 TTTCGACAGAGCTGCTGAGCTAAGACATCTGCAATTTGTAAGTAAAGCCACGAGTTG 148

Qy 232 GTGAGAGAGACCTCAGAACTTCTATACCTTTGTTATGGTGAATCCAGATTTCCAACTC 291

Db 149 GTGCGAGTACATAGAGTTCTACACACCGCTGATATTTGTTGAGATCCAGACGCTCCAAAGCC 208

Qy 292 CTAGAACCTTCACCTCCGAGAAATATCTCATTTGGTTGGTGAATGATATCCCTGTACAA 351

Db 209 CAGTACACCTTCACCTAAGGAGATCTTGCATGTGATGTGTACAGACTCCCTGGAAACA 268

Qy 352 CTGGAACAACCTTTGGCAATGAGATTTGTGTAGAAATCCAAATCCCACTCAGAGAA 411

Db 269 CTGGGCGCAGCTTGGCGCCGAGAGCTTTAGTTTATGAAAGACAGAAACCAAGATCTGTA 328

Qy 412 TTTCATGCTGTGTTTATATTTTTCAGACCTTTGGCAGCAACAGATGATGACCAAG 471

Db 329 TCCACCGGATGATTTGTGCTGTTCCAGCAACTAGGAGGATACATTTTGTGACCAAG 388

Qy 472 GGTGGCGCCAGACACTTCAACACTGCGAGTTTGTGATCTACAAATCTCGGCTTCCG 531

Db 389 ACGTCCGACAAACTTTCAGCTGCAGAGAACTTTGCACGCGAGTACCACTTAACGTT---G 445

Qy 532 TGGCGCAGTTTCTACAAATTTGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTT 587

Db 446 TGGCTGCTCATATTTTCAACTGTCAAGGAGAGGTGATCAGCGGAGAGAGTTT 501

RESULT 15

BJ315664

LOCUS BJ315664 597 bp mRNA linear EST 09-APR-2002

DEFINITION BJ315664 Y. Ogihara unpublished cDNA library, Wh_yf Triticum

aestivum cDNA clone whyf19117 5', mRNA sequence.

ACCESSION BJ315664

VERSION BJ315664

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 597)

AUTHORS Ogihara, Y. and Murai, K.

TITLE Expressed genes in Triticum aestivum

JOURNAL Unpublished (2002)

COMMENT Contact: Tadasu Shin-i

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

FEATURES

Location/Qualifiers

1..597

source

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="whyf19117"

/clone_id="Y. Ogihara unpublished cDNA library, Wh_yf"

/tissue_type="spikelet at early flowering"

/dev_stage="Peekes' scale 6"

/note="Vector: lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T7 Close Lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 153 a 151 c 143 g 147 t 3 others

ORIGIN

Query Match 18.4%: Score 157.2; DB 13; Length 597;

Best Local Similarity 59.0%: Pred. No. 9.4e-18;

Matches 289; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

OY	81	GACCCCTTTATAGTAAGACAGAGTGGTGGAGACGCTCTGTATCCGTTATTAATAGTCAATC	140
Db	83	GAACCTCTTATTTGGGGGGGGGTATTGGAGAAAGTTCTTGATACATTAAACCACTGGTG	142
OY	141	ACTCTAAAGGTTACTTATGAGCCAAAGAGAG--GTGACTAATAGGCTTGGATCTAAGGCGCT	197
Db	143	AAGATGGTAAAGACCTTATTACTCCAAAGCTTGTCTTCAATGGCCATGAGCTCTACCCA	202
OY	198	TCTAGAGTTCAAAACAAGCCCAAGAGTTGAGTGGTGGAGAAAGCCACAGAACTCTAT	257
Db	203	TCAGCGGTTGATCTAAACCAACGATGAGAGTCCCAAGGGGTGACTTGGCATCTTGTTTC	262
OY	258	ACTTTGGTTATGGTGAGATCCAGATGTTTCCAAGTCTTAGCAACCTCCACTCGAGAAATAT	317
Db	263	ACACGCGTTATGACAGACACCTGATGTGCCAGGGCCAGATGATCATATCTAAAGGAGCAC	322
OY	318	CTCCATTTGGTGGAGCTGATATCCCGTACCTGATCAACCTGAGAACCACTTGGCATAGATT	377
Db	323	CTTCACTGATTTGTTACTGATATATACCTGGACACACAGATGCTTCTTTTGGACGGGAATC	382
OY	378	GTTGTTTACGAAAAATCCAAAGTCCACATGCAACAGAAATTCATGTCGTGTTTATATTGTTT	437
Db	383	ATAAGCTTATGAGACCCCAAAACCCAAATGAGCATCCACAGGTTCAATTTTTTGGTCTCTTC	442
OY	438	CGACAGCTTGGCAGGCAAAACGTATATGCACACAGGGTGGGGCCAGAACTTCAACACTCGC	497
Db	443	AAGCAGAAAGCCAGACAGACTGTAACGTGTGCTTCTTTCAGGGATCTATTTCACACACCCGT	502
OY	498	GAGTTTGGCTGAGATCTCAAAATCTTGCGCTTCCGTGGCCACAGTTTCTCAATTGTCAG	557
Db	503	CAGTTTGGCTGGAGAAATGACCTCGGCTCCCTGTGCACACTGTCTCACTTCAACTGTCA	562
OY	558	AGGGAAGTGTG	567
Db	563	AGGGAAGTGTG	572

Search completed: May 2, 2003, 11:50:30
Job time : 1791.5 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 15:58:02 ; Search time 60 seconds
(without alignments)
4375.255 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856
Sequence: 1 tctagaactagtgatgccccc.....aaaaaaaaaactcgcag 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA:*
1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCRTOS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/Backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	856	100.0	856	US-09-060-726A-3	Sequence 3, Appl1
2	842.4	98.4	855	US-09-060-726A-1	Sequence 1, Appl1
3	71.8	8.4	822	US-07-644-372-1	Sequence 1, Appl1
C 4	47	5.5	2185	US-08-467-948A-3	Sequence 3, Appl1
5	47	5.5	2185	US-08-467-947A-3	Sequence 3, Appl1
6	46.8	5.5	234	US-08-485-455D-60	Sequence 60, Appl1
7	46.8	5.5	234	US-08-482-130C-60	Sequence 60, Appl1
8	46.8	5.5	234	US-08-484-211C-60	Sequence 60, Appl1
9	46.8	5.5	234	US-08-906-769-60	Sequence 60, Appl1
10	46.8	5.5	234	US-08-906-616-60	Sequence 60, Appl1
11	46.8	5.5	234	US-08-817-795-60	Sequence 60, Appl1
12	46.8	5.5	234	US-08-485-443B-60	Sequence 60, Appl1
13	46.8	5.5	234	US-08-639-075A-60	Sequence 60, Appl1
14	46.8	5.5	234	US-09-012-431-60	Sequence 60, Appl1
15	46.8	5.5	234	US-09-012-692-60	Sequence 60, Appl1
16	46.8	5.5	234	US-08-906-613-60	Sequence 60, Appl1
17	46.8	5.5	234	PCR-US85-14442A-60	Sequence 60, Appl1
18	45.6	5.3	1601	US-07-968-971A-10	Sequence 10, Appl1
19	45.6	5.3	1601	US-08-424-406-6	Sequence 6, Appl1
20	45.4	5.3	2503	US-08-472-934-3	Sequence 3, Appl1
21	45.4	5.3	2503	US-08-472-934-11	Sequence 11, Appl1
22	45.4	5.3	2503	US-08-472-934-11	Sequence 11, Appl1
23	45.4	5.3	2503	US-08-461-146C-3	Sequence 3, Appl1
24	45.4	5.3	2503	US-08-461-146C-11	Sequence 11, Appl1
25	45.4	5.3	2503	US-08-461-145C-3	Sequence 3, Appl1
26	45.4	5.3	2503	US-08-461-145C-11	Sequence 11, Appl1
27	45.4	5.3	2503	US-08-628-829-5	Sequence 5, Appl1

28	45.4	5.3	2503	US-08-628-829-7	Sequence 7, Appl1
29	45	5.3	1585	US-09-183-861-54	Sequence 54, Appl1
30	45	5.3	1585	US-09-022-765-54	Sequence 54, Appl1
31	44.8	5.2	897	US-08-899-330-14	Sequence 14, Appl1
32	44.8	5.2	3328	US-08-960-048-1	Sequence 1, Appl1
33	44.6	5.2	545	US-09-227-357-125	Sequence 125, Appl1
34	44.4	5.2	866	US-09-257-179-11	Sequence 11, Appl1
35	43.8	5.1	1058	US-08-818-112-14	Sequence 14, Appl1
36	43.8	5.1	1058	US-08-818-111-14	Sequence 14, Appl1
37	43.8	5.1	1058	US-09-056-556-14	Sequence 14, Appl1
38	43.8	5.1	1058	US-09-072-596-14	Sequence 14, Appl1
39	43.8	5.1	2775	US-08-730-771-1	Sequence 1, Appl1
40	43.8	5.1	2775	US-09-060-208-1	Sequence 1, Appl1
41	43.6	5.1	860	US-08-181-271A-33	Sequence 33, Appl1
42	43.6	5.1	860	US-08-449-315-33	Sequence 33, Appl1
43	43.6	5.1	860	US-08-444-803-33	Sequence 33, Appl1
44	43.6	5.1	860	US-08-449-043-33	Sequence 33, Appl1
45	43.6	5.1	860	US-08-456-265A-33	Sequence 33, Appl1

ALIGNMENTS

```
RESULT 1
US-09-060-726A-3/C
; Sequence 3, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS.026A
; CURRENT APPLICATION NUMBER: US/09/060.726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-060-726A-3

Query Match      100.0%; Score 856; DB 4; Length 856;
Best Local Similarity 100.0%; Pred. No. 3e-217;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGTGATCCCGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
    |||||||
DB 856 TCTAGACTAGTGTGATCCCGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 797
    |||||||

QY 61 AGATGCTATAAATATTAAGACCCCTTATAGTAAGCAGAGTTGAGACGTTCTTG 120
    |||||||
DB 796 AGATGCTATAAATATTAAGACCCCTTATAGTAAGCAGAGTTGAGACGTTCTTG 737
    |||||||

QY 121 ATCGTTTATAGTCAATCACTTAAGTTACTTATGSCCAAGAGAGTACTATG 180
    |||||||
DB 736 ATCGTTTATAGTCAATCACTTAAGTTACTTATGSCCAAGAGAGTACTATG 677
    |||||||

QY 181 GCTTGATCTAAGGCTTCAGGTTCAAAACCAAGAGTTGATGTTGGAAGAAG 240
    |||||||
DB 676 GCTTGATCTAAGGCTTCAGGTTCAAAACCAAGAGTTGATGTTGGAAGAAG 617
    |||||||

QY 241 ACTCAGGAACCTTATATCTTGTATGTTGATGATCCAGATGTTCAAGTCTAGCAACC 300
    |||||||
DB 616 ACTCAGGAACCTTATATCTTGTATGTTGATGATCCAGATGTTCAAGTCTAGCAACC 557
    |||||||

QY 301 CTCACCTCCAGAAATATCTCATGTTGTTGATGATGATATCCGTTACAACTGACAA 360
    |||||||
DB 556 CTCACCTCCAGAAATATCTCATGTTGTTGATGATGATATCCGTTACAACTGACAA 497
    |||||||

QY 361 CCTTTGCAATGATGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATG 420
    |||||||
```

Db 496 CCTTGGCAATGATGTTGTTACGAAAATCCAGTCCCACTGAGGAATTCATCGTG 437
Oy 421 TCGTGTATATATGTTTCCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 480
Db 436 TCGTGTATATGTTTCCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 377
Oy 481 AGACTTCAACACTGCGGAGTTTGTGAGATCTACAACTCGGCTTCCCGTGGCCGAG 540
Db 376 AGAACTTCAACACTGCGGAGTTTGTGAGATCTACAACTCGGCTTCCCGTGGCCGAG 317
Oy 541 TTTTTCACAACTGTCAGAGAGAGTGGCTGGGAGAGAAAGACTTTAGATGGCTTCT 600
Db 316 TTTTTCACAACTGTCAGAGAGAGTGGCTGGGAGAGAAAGACTTTAGATGGCTTCT 257
Oy 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 256 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 197
Oy 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 196 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137
Oy 721 TATAAGTGTAG 780
Db 136 TATAAGTGTAG 77
Oy 781 TGTGATGCGAT 840
Db 76 TGTGATGCGAT 17
Oy 841 AAAAAAAAAAATCTGAG 856
Db 16 AAAAAAAAAAATCTGAG 1

RESULT 2
US-09-060-726A-1
; Sequence 1, Application US/09060726A
; Patent No. 6225350
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; FILE REFERENCE: SALKINS: 026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(590)
US-09-060-726A-1

Query Match 98.4%; Score 842.4; DB 4; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-213;
Matches 854; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 1 TCTAGACATAGTATCCCGCGGCTGAGAAATTCAGACAGAGTTTCTCAAGATCAA 60
Db 1 TCTAGACATAGTATCCCGCGGCTGAGAAATTCAGACAGAGTTTCTCAAGATCAA 60
Oy 61 AGATGCTATATATATATAGAGACCTCTTATATAGACAGAGTTTGGAGAGCTTCTG 120
Db 61 AGATGCTATATATATATAGAGACCTCTTATATAGAGAGAGTTTGGAGAGCTTCTG 120
Oy 121 ATCGGTTAATGATCATCATCTAAAGGTTACTTATGCGCAAGAGAGGATCAATG 180
Db 121 ATCGGTTAATGATCATCATCTAAAGGTTACTTATGCGCAAGAGAGGATCAATG 180

Oy 181 GCTTGATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAGAGTGTGATTTGGTGAAG 240
Db 181 GCTTGATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAGAGTGTGATTTGGTGAAG 240
Oy 241 ACCTCAGAACTTCTATCTTGTGTTATGTTGATTCAGATGTTCCAGTCTAGCAAC 300
Db 241 ACCTCAGAACTTCTATCTTGTGTTATGTTGATTCAGATGTTCCAGTCTAGCAAC 300
Oy 301 CTCACCTCGAGAAATTCCTCAGTGGTGGTGTGATGATGATGATGATGATGATGAT 360
Db 301 CTCACCTCGAGAAATTCCTCAGTGGTGGTGTGATGATGATGATGATGATGATGAT 360
Oy 361 CCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Oy 421 TCGTGTATATATGTTTCCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 480
Db 421 TCGTGTATATATGTTTCCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 480
Oy 481 AGAACTTCAACACTGCGGAGTTTGTGAGATCTACAACTCGGCTTCCCGTGGCCGAG 540
Db 481 AGAACTTCAACACTGCGGAGTTTGTGAGATCTACAACTCGGCTTCCCGTGGCCGAG 540
Oy 541 TTTTTCACAACTGTCAGAGAGAGTGGCTGGGAGAGAAAGACTTTAGATGGCTTCT 600
Db 541 TTTTTCACAACTGTCAGAGAGAGTGGCTGGGAGAGAAAGACTTTAGATGGCTTCT 600
Oy 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659
Oy 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
Oy 721 TATAAGTGTAG 780
Db 721 TATAAGTGTAG 779
Oy 781 TGTGATGCGAT 840
Db 781 TGTGATGCGAT 839
Oy 841 AAAAAAAAAAATCTGAG 856
Db 841 AAAAAAAAAAATCTGAG 855

RESULT 3
US-07-644-372-1
; Sequence 1, Application US/07644372
; Patent No. 5416009
; GENERAL INFORMATION:
; APPLICANT: Lazzeri, Mario E.
; APPLICANT: Nutman, Thomas B.
; APPLICANT: Weiss, Nikolaus
; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-947A-3

Query Match
Best Local Similarity 5.5%; Score 47; DB 3; Length 2185;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGACGAGTTTGTTCAG 55
DB 2072 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGGAGTTGGTTGAG 2018

RESULT 6
US-08-485-455D-60
Sequence 60, Application US/08485455D
Patent No. 5712143
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Slegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/485,455D
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-455D-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 1; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGACGAGTTTGTTCAGATCA 60
DB 48 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGACGAGTTTGTTCAGATCA 107

QY 61 AGATGCTAATAATATAGAGA 82
DB 108 GCGCGTCTCATCTTACAGATA 129

RESULT 7
US-08-482-130C-60
Sequence 60, Application US/08482130C
Patent No. 5962257
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Slegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/482,130C
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-482-130C-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 2; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTGATTTGA 107
QY 61 AGATGCTATAATAATATAAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAAGATA 129

RESULT 8

US-08-484-211C-60
; Sequence 60, Application US/08484211C
; Patent No. 5972645
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary L.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,211C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..234
US-08-484-211C-60
Query Match 5.5%; Score 46.8; DB 2; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTGATTTGA 107
QY 61 AGATGCTATAATAATATAAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAAGATA 129

RESULT 9
US-08-906-769-60
; Sequence 60, Application US/08906769

; Patent No. 6077687
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Silver, Gary
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,769
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,075
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..234
US-08-906-769-60
Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGACTAGTGCATCCCGGCTGCAGGATTCACAGAGGTTGTTGATTTGA 107
QY 61 AGATGCTATAATAATATAAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAAGATA 129

RESULT 10
US-08-906-616-60
; Sequence 60, Application US/08906616
; Patent No. 6121035
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary

APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-906-616-60

Query Match
Best local similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTCAAGATCAA 60
DB 48 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTGATTTGA 107
QY 61 AGATGCTCTAATAATATAAGAGA 82
DB 108 GCGCGTCTCATCTTACAGAGATA 129

RESULT 11
US-08-817-795-60
Sequence 60, Application US/08817795
Patent No. 6139840
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Miles Yamataka
APPLICANT: Afstien, Ann
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-817-795-60

Query Match
Best local similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTCAAGATCAA 60
DB 48 TCTAGACTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTGATTTGA 107
QY 61 AGATGCTCTAATAATATAAGAGA 82
DB 108 GCGCGTCTCATCTTACAGAGATA 129

RESULT 12
US-08-485-443B-60
Sequence 60, Application US/08485443B
Patent No. 6146870
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,443B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
TELEFAX: 303 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-443B-60

Query Match
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCACGACGAGTTGTTCAGATCAA 60
|||||
Db 48 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCGCGACGAGCGTTGGTTGATTTGA 107

OY 61 AGATGCTATAATATATAGAGA 82
|||||
Db 108 GCGCCTCATCTTACAGAGATA 129

RESULT 13
US-08-639-075A-60
Sequence 60, Application US/08639075A
Patent No. 6150125
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

Query Match
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCACGACGAGTTGTTCAGATCAA 60
|||||
Db 48 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCGCGACGAGCGTTGGTTGATTTGA 107

OY 61 AGATGCTATAATATATAGAGA 82
|||||
Db 108 GCGCCTCATCTTACAGAGATA 129

RESULT 14
US-09-012-431-60
Sequence 60, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-012-431-60

Query Match 5.5%; Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCGCGCAGAGCGTTGTTGATGA 107
QY 61 AGATGCTATATAATATAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAGATA 129

RESULT 15

US-09-012-692-60
Sequence 60, Application US/09012692
Patent No. 6214579

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,692

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:

LENGTH: 234 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..234

US-09-012-692-60

Query Match 5.5%; Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCGCGCAGAGCGTTGTTGATGA 107
QY 61 AGATGCTATATAATATAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAGATA 129

Search completed: May 1, 2003, 21:56:13
Job time : 65 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 15:58:02 ; Search time 156.5 Seconds

(without alignments)
6463.052 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856

Sequence: 1 tctagactagctgtagctccccc.....aaaaaaaaaaactcgcgag 856

Scoring table: IDENTITY_NUC

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCrUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	856	100.0	856	US-09-291-809C-1	Sequence 1, Appl1
2	856	100.0	856	US-09-291-809C-3	Sequence 3, Appl1
3	856	100.0	856	US-09-845-849-1	Sequence 1, Appl1
4	856	100.0	856	US-09-845-849-3	Sequence 3, Appl1
5	377.6	44.1	856	US-09-938-842A-2635	Sequence 2635, App
6	176.8	20.7	534	US-09-938-842A-1501	Sequence 1501, App
7	74.2	8.7	251	US-09-878-574-6398	Sequence 6398, App
8	49.2	5.7	503	US-10-092-154-380	Sequence 380, App
9	49.2	5.7	367	US-10-074-095-248	Sequence 248, App
10	48.2	5.6	367	US-10-074-095-248	Sequence 248, App
11	48.2	5.6	367	US-09-764-860-248	Sequence 248, App
12	48.2	5.6	367	US-09-925-300-816	Sequence 816, App
13	47.8	5.6	2585	US-09-764-868-303	Sequence 303, App
14	47.6	5.6	560	US-09-925-297-400	Sequence 400, App
15	47.6	5.6	631	US-09-764-891-404	Sequence 404, App
16	47.4	5.5	485	US-09-764-891-2323	Sequence 2323, App
17	47.4	5.5	515	US-09-925-299-270	Sequence 270, App
18	47.4	5.5	515	US-09-925-299-270	Sequence 270, App
19	47.4	5.5	1479	US-10-097-065-96	Sequence 96, Appl1

20	47	5.5	2185	9	US-10-024-494-3	Sequence 3, Appl1
21	46.8	5.5	559	9	US-09-925-299-309	Sequence 309, App
22	46.8	5.5	559	10	US-09-925-299-309	Sequence 309, App
23	46.8	5.5	577	10	US-09-764-864-235	Sequence 235, App
24	46.8	5.5	632	9	US-09-925-299-352	Sequence 352, App
25	46.8	5.5	632	10	US-09-925-299-352	Sequence 352, App
26	46.8	5.5	1711	9	US-09-983-204-3	Sequence 3, Appl1
27	46.8	5.5	2458	10	US-09-764-864-78	Sequence 78, App
28	46.6	5.4	609	9	US-09-764-891-403	Sequence 403, App
29	46.4	5.4	481	9	US-09-988-442-293	Sequence 293, App
30	46.4	5.4	612	9	US-10-091-438-103	Sequence 103, App
31	46.4	5.4	612	10	US-09-764-853-349	Sequence 349, App
32	46.2	5.4	812	9	US-09-986-480-48	Sequence 48, Appl1
33	46.2	5.4	2787	10	US-09-764-864-412	Sequence 412, App
34	46	5.4	741	9	US-10-125-540-184	Sequence 184, App
35	46	5.4	741	10	US-09-764-870-184	Sequence 184, App
36	45.8	5.4	608	9	US-09-776-724A-39	Sequence 39, Appl1
37	45.8	5.4	726	9	US-09-986-480-36	Sequence 36, Appl1
38	45.8	5.4	1116	9	US-09-764-868-341	Sequence 341, App
39	45.8	5.4	1753	10	US-09-764-864-774	Sequence 774, App
40	45.8	5.4	2554	10	US-09-764-864-352	Sequence 352, App
41	45.6	5.3	707	10	US-09-764-864-706	Sequence 706, App
42	45.6	5.3	1035	10	US-09-739-907-16	Sequence 16, Appl1
43	45.6	5.3	1712	10	US-09-925-300-643	Sequence 643, App
44	45.4	5.3	565	10	US-09-925-301-611	Sequence 611, App
45	45.4	5.3	597	10	US-09-925-300-843	Sequence 843, App

ALIGNMENTS

```

RESULT 1
US-09-291-809C-1
; Sequence 1, Application US/09291809C
; Patent No. US20010049831A1
; GENERAL INFORMATION:
; APPLICANT: Dettlef Weigel
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SLKINS: 026CPI
; CURRENT APPLICATION NUMBER: US/09/291,809C
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: PCT/US99/08151
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(588)
US-09-291-809C-1
Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGAGATTGTGGAGAG 240
    |||||
Db 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGAGATTGTGGAGAG 240
Qy 241 ACCTCAGGAACCTCTACTTCTGTTATGATGATCCAGATGTTCCAAAGTCTCAGAAC 300
    |||||
Db 241 ACCTCAGGAACCTCTACTTCTGTTATGATGATCCAGATGTTCCAAAGTCTCAGAAC 300
Qy 301 CTCACCTCCGAGAAATCTCCATTTGGTGGTGCATGATATCCCTGGTACAACTGSAACA 360
    |||||
Db 301 CTCACCTCCGAGAAATCTCCATTTGGTGGTGCATGATATCCCTGGTACAACTGSAACA 360
Qy 361 CCTTTGGCAATGAGATGTGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
    |||||
Db 361 CCTTTGGCAATGAGATGTGTGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
Qy 421 TCGTGTATATTTGTTTCCAGAGCTTGGCAGGCAAGAGTATGCAACAGGTTGGCCGC 480
    |||||
Db 421 TCGTGTATATTTGTTTCCAGAGCTTGGCAGGCAAGAGTATGCAACAGGTTGGCCGC 480
Qy 481 AGAAGCTTCAACACTCCGAGTTTGTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
    |||||
Db 481 AGAAGCTTCAACACTCCGAGTTTGTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
Qy 541 TTTTTCACAAATTTGTCAAGAGGAGAGTGGCTGGCGAGAAAGACTTTAGATGGCTTCT 600
    |||||
Db 541 TTTTTCACAAATTTGTCAAGAGGAGAGTGGCTGGCGAGAAAGACTTTAGATGGCTTCT 600
Qy 601 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 660
    |||||
Db 601 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 660
Qy 661 TTTTAAATACCAATTTATTTATGATAGAGTAACAGAGTATGATGATGATGATGATGAT 720
    |||||
Db 661 TTTTAAATACCAATTTATTTATGATAGAGTAACAGAGTATGATGATGATGATGATGAT 720
Qy 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTATATAGTG 780
    |||||
Db 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTATATAGTG 780
Qy 781 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATATTTTAAAAA 840
    |||||
Db 781 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATATTTTAAAAA 840
Qy 841 AAAAAAAAAAATCTCGAG 856
    |||||
Db 841 AAAAAAAAAAATCTCGAG 856

RESULT 2
; Sequence 3, Application US/09291809C
; Patent No. US20010049831A1
; GENERAL INFORMATION:
; APPLICANT: Delfel Weigel
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; FILE REFERENCE: SALKINS 026CP1
; CURRENT APPLICATION NUMBER: US/09/291,809C
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: PCT/US99/08151
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-291-809C-3
```

```
Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTAGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
    |||||
Db 856 TCTAGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Qy 61 AGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
    |||||
Db 796 AGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
Qy 121 ATCCGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
    |||||
Db 736 ATCCGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGAGATTGTGGAGAG 240
    |||||
Db 676 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGAGATTGTGGAGAG 240
Qy 241 ACCTCAGGAACCTCTACTTCTGTTATGATGATCCAGATGTTCCAAAGTCTCAGAAC 300
    |||||
Db 616 ACCTCAGGAACCTCTACTTCTGTTATGATGATCCAGATGTTCCAAAGTCTCAGAAC 300
Qy 301 CTCACCTCCGAGAAATCTCCATTTGGTGGTGCATGATATCCCTGGTACAACTGSAACA 360
    |||||
Db 556 CTCACCTCCGAGAAATCTCCATTTGGTGGTGCATGATATCCCTGGTACAACTGSAACA 360
Qy 361 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 420
    |||||
Db 496 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 420
Qy 421 TCGTGTATATTTGTTTCCAGAGCTTGGCAGGCAAGAGTATGCAACAGGTTGGCCGC 480
    |||||
Db 436 TCGTGTATATTTGTTTCCAGAGCTTGGCAGGCAAGAGTATGCAACAGGTTGGCCGC 480
Qy 481 AGAAGCTTCAACACTCCGAGTTTGTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
    |||||
Db 376 AGAAGCTTCAACACTCCGAGTTTGTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
Qy 541 TTTTTCACAAATTTGTCAAGAGGAGAGTGGCTGGCGAGAAAGACTTTAGATGGCTTCT 600
    |||||
Db 316 TTTTTCACAAATTTGTCAAGAGGAGAGTGGCTGGCGAGAAAGACTTTAGATGGCTTCT 600
Qy 601 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 660
    |||||
Db 256 CCTTTTAAACAATTTATTTGATCTGATGATGATTTATCTATCTATAGATTATTA 660
Qy 661 TTTTAAATACCAATTTATTTATGATAGAGTAACAGAGTATGATGATGATGATGATGAT 720
    |||||
Db 196 TTTTAAATACCAATTTATTTATGATAGAGTAACAGAGTATGATGATGATGATGATGAT 720
Qy 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTATATAGTG 780
    |||||
Db 136 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTATATAGTG 780
Qy 781 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATATTTTAAAAA 840
    |||||
Db 76 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATATTTTAAAAA 840
Qy 841 AAAAAAAAAAATCTCGAG 856
    |||||
Db 16 AAAAAAAAAAATCTCGAG 1

RESULT 3
; Sequence 1, Application US/09845849
; Patent No. US20020029395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WEIGEL, Delfel
US-09-845-849-1
```

```
APPLICANT: KARDALISKY, Igor
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS-026DVI
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-845-849-1

Query Match      100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTTGTCAAGATCAA 60
    |||||||
DB 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTTGTCAAGATCAA 60

QY 61 AGATGCTATAAATATAAGAGACCCCTTATAGTAAAGAGAGTTGGAGACGTTCTTG 120
    |||||||
DB 61 AGATGCTATAAATATAAGAGACCCCTTATAGTAAAGAGAGTTGGAGACGTTCTTG 120

QY 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAGAGAGTGAATATG 180
    |||||||
DB 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAGAGAGTGAATATG 180

QY 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAAACAAGCCAGAGTTGAGATTGGAGAG 240
    |||||||
DB 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAAACAAGCCAGAGTTGAGATTGGAGAG 240

QY 241 ACCTCAGGAAGTCTTACTTGTGTATGAGTGATCCAGATGTTCCAAAGTCTGCAACC 300
    |||||||
DB 241 ACCTCAGGAAGTCTTACTTGTGTATGAGTGATCCAGATGTTCCAAAGTCTGCAACC 300

QY 301 CTCACCTCCGAGAAATATCTCCATTGGTTGTGACTGATATCCCTGCTACAACTGGAACAA 360
    |||||||
DB 301 CTCACCTCCGAGAAATATCTCCATTGGTTGTGACTGATATCCCTGCTACAACTGGAACAA 360

QY 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACGACGAGATTTATGCTG 420
    |||||||
DB 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACGACGAGATTTATGCTG 420

QY 421 TCGGTATTATATGTTTTCGACAGCTTGGCAGGCAAAACAGTATGCAACAGGATGCGCC 480
    |||||||
DB 421 TCGGTATTATATGTTTTCGACAGCTTGGCAGGCAAAACAGTATGCAACAGGATGCGCC 480

QY 481 AGAAGCTCAACACTCGGAGTTTGTGAGATCTACAAATCTCCGCTCCGCGCGAG 540
    |||||||
DB 481 AGAAGCTCAACACTCGGAGTTTGTGAGATCTACAAATCTCCGCTCCGCGCGAG 540

QY 541 TTTTCTCAATFTGTCAGAGGAGAGTGGCTGCGAGAGAAAGACTTTAGTGGCTTCTT 600
    |||||||
DB 541 TTTTCTCAATFTGTCAGAGGAGAGTGGCTGCGAGAGAAAGACTTTAGTGGCTTCTT 600

QY 601 CCTTTAATACCAATTTGATGATGAGATGAGATTTTATGATCTATATGTTTAA 660
    |||||||
DB 601 CCTTTAATACCAATTTGATGATGAGATGAGATTTTATGATCTATATGTTTAA 660

QY 661 TTTAATAACCAATTTTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 720
    |||||||
DB 661 TTTAATAACCAATTTTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 720

QY 721 TATAGAGTGTATATAAATAAGAGGAGGAGGAGAAATGAGAGTGTATTACTATATAGTG 780
    |||||||
DB 721 TATAGAGTGTATATAAATAAGAGGAGGAGGAGAAATGAGAGTGTATTACTATATAGTG 780

QY 781 TGTGATCGAATATATATATTAATCTACATGAATGAAGTGTATATATATAAAAAAAA 840
    |||||||
```

```
|||||
DB 781 TGTATCGAATATATATATATCTACATGAATGAAGTGTATATATATAAAAAAAA 840

QY 841 AAAAAAAAAAACTCGAG 856
    |||||||
DB 841 AAAAAAAAAAACTCGAG 856

RESULT 4
US-09-845-849-3/c
Sequence 3, Application US/09845849
Patent No. US20020029395A1
GENERAL INFORMATION:
APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
APPLICANT: WEGEL, David
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS-026DVI
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-845-849-3

Query Match      100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTTGTCAAGATCAA 60
    |||||||
DB 856 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTTGTCAAGATCAA 60

QY 61 AGATGCTATAAATATAAGAGACCCCTTATAGTAAAGAGAGTTGGAGACGTTCTTG 120
    |||||||
DB 61 AGATGCTATAAATATAAGAGACCCCTTATAGTAAAGAGAGTTGGAGACGTTCTTG 120

QY 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAGAGAGTGAATATG 180
    |||||||
DB 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAGAGAGTGAATATG 180

QY 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAAACAAGCCAGAGTTGAGATTGGAGAG 240
    |||||||
DB 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAAACAAGCCAGAGTTGAGATTGGAGAG 240

QY 241 ACCTCAGGAAGTCTTACTTGTGTATGAGTGATCCAGATGTTCCAAAGTCTGCAACC 300
    |||||||
DB 241 ACCTCAGGAAGTCTTACTTGTGTATGAGTGATCCAGATGTTCCAAAGTCTGCAACC 300

QY 301 CTCACCTCCGAGAAATATCTCCATTGGTTGTGACTGATATCCCTGCTACAACTGGAACAA 360
    |||||||
DB 301 CTCACCTCCGAGAAATATCTCCATTGGTTGTGACTGATATCCCTGCTACAACTGGAACAA 360

QY 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACGACGAGATTTATGCTG 420
    |||||||
DB 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACGACGAGATTTATGCTG 420

QY 421 TCGGTATTATATGTTTTCGACAGCTTGGCAGGCAAAACAGTATGCAACAGGATGCGCC 480
    |||||||
DB 421 TCGGTATTATATGTTTTCGACAGCTTGGCAGGCAAAACAGTATGCAACAGGATGCGCC 480

QY 481 AGAAGCTCAACACTCGGAGTTTGTGAGATCTACAAATCTCCGCTCCGCGCGAG 540
    |||||||
DB 481 AGAAGCTCAACACTCGGAGTTTGTGAGATCTACAAATCTCCGCTCCGCGCGAG 540

QY 541 TTTTCTCAATFTGTCAGAGGAGAGTGGCTGCGAGAGAAAGACTTTAGTGGCTTCTT 600
    |||||||
```


Query Match	5.7%	Score 49.2	DB 10	Length 503
Best Local Similarity	81.4%	Pred. No. 0.01		
Matches 57	Conservative 0	Mismatches 13	Indels 0	Gaps 0

07 1 TCTAAACTAGTGGATCCCCGGGCTGCAGGAAATTCAGCAGCAGGTTTGTTCACAGTCAA 60
 |||||

Db 76 TCTAGACTAGTGATCCCGGCGCTGCAGAAATTCGCGACGAGTTTATTATTATTTTA 135
 QY 61 AGATGCTAT 70
 Db 136 TGGGCTTTT 145

RESULT 10
 US-10-074-095-248/c
 ; Sequence 248, Application US/10074095
 ; Publication No. US20030077704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC008C1
 ; CURRENT APPLICATION NUMBER: US/10/074,095
 ; CURRENT FILING DATE: 2002-02-14
 ; PRIOR APPLICATION NUMBER: 09/764,860
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,447
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/218,290
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/225,757
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,267
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/216,880
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/251,869
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/235,834
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/234,274
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/234,223
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/228,924
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/224,518
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,369
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/224,519
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,964
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/241,809
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/249,299
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/236,327
 ; PRIOR FILING DATE: 2000-09-29

;; PRIOR APPLICATION NUMBER: 60/241,785
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/244,617
 ;; PRIOR FILING DATE: 2000-11-01
 ;; PRIOR APPLICATION NUMBER: 60/225,268
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/236,368
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/251,856
 ;; PRIOR FILING DATE: 2000-12-08
 ;; PRIOR APPLICATION NUMBER: 60/251,868
 ;; PRIOR FILING DATE: 2000-12-08
 ;; PRIOR APPLICATION NUMBER: 60/229,344
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/234,997
 ;; PRIOR FILING DATE: 2000-09-25
 ;; PRIOR APPLICATION NUMBER: 60/229,343
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,345
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,287
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,513
 ;; PRIOR FILING DATE: 2000-09-05
 ;; PRIOR APPLICATION NUMBER: 60/231,413
 ;; PRIOR FILING DATE: 2000-09-08
 ;; PRIOR APPLICATION NUMBER: 60/229,509
 ;; PRIOR FILING DATE: 2000-09-05
 ;; PRIOR APPLICATION NUMBER: 60/236,367
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/237,039
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,038
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/236,370
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/236,802
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,037
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,040
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/240,960
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/239,935
 ;; PRIOR FILING DATE: 2000-10-13
 ;; PRIOR APPLICATION NUMBER: 60/239,937
 ;; PRIOR FILING DATE: 2000-10-13
 ;; PRIOR APPLICATION NUMBER: 60/241,787
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/246,474
 ;; PRIOR FILING DATE: 2000-11-08
 ;; PRIOR APPLICATION NUMBER: 60/246,532
 ;; PRIOR FILING DATE: 2000-11-08
 ;; PRIOR APPLICATION NUMBER: 60/249,216
 ;; PRIOR FILING DATE: 2000-11-17
 ;; PRIOR APPLICATION NUMBER: 60/249,210
 ;; PRIOR FILING DATE: 2000-11-17
 ;; PRIOR APPLICATION NUMBER: 60/226,681
 ;; PRIOR FILING DATE: 2000-08-22
 ;; PRIOR APPLICATION NUMBER: 60/225,759
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/225,213
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/227,182
 ;; PRIOR FILING DATE: 2000-08-22
 ;; PRIOR APPLICATION NUMBER: 60/225,214
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/235,836
 ;; PRIOR FILING DATE: 2000-09-27
 ;; PRIOR APPLICATION NUMBER: 60/230,438
 ;; PRIOR FILING DATE: 2000-09-06
 ;; PRIOR APPLICATION NUMBER: 60/215,135

```

: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 60/225,266
: PRIOR FILING DATE: 2000-08-14
: PRIOR APPLICATION NUMBER: 60/249,218
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,208
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,213
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,212
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,207
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,245
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,244
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,217
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,211
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,215
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,264
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,214
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,297
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/232,400
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/231,242
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,081
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,080
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,414
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,244
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/233,064
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/233,063
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,397
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,399
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,401
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/241,808
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,826
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,786
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,221
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/246,475
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: 60/231,243
: PRIOR FILING DATE: 2000-09-08

```

```

Query Match          5.6%; Score 48.2; DB 9; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 1 TCTAGACTAGTGGATCCCGGCGCTGCAGAAATTCAGCAGAGTTTTCAGATCAA 60
    |||||
DB 305 TCTAGAACTAGTGGATCCCGGCGCTGCAGAAATTCAGCAGAGTTTTCAGATCAA 246
QY 61 AGATGCTATATAATAATA 77

```

```

DB 245 TATCTTTTATGACACA 229

```

```

RESULT 11
US-09-764-860-248/c
: Sequence 248, Application US/09764860
: Patent No. US20020094953A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC008
: CURRENT APPLICATION NUMBER: US/09/764,860
: PRIOR FILING DATE: 2001-01-17
: NUMBER OF SEQ ID NOS: 1198
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 248
: LENGTH: 367
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (345)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-248

```

```

Query Match          5.6%; Score 48.2; DB 10; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 1 TCTAGACTAGTGGATCCCGGCGCTGCAGAAATTCAGCAGAGTTTTCAGATCAA 60
    |||||
DB 305 TCTAGAACTAGTGGATCCCGGCGCTGCAGAAATTCAGCAGAGTTTTCAGATCAA 246
QY 61 AGATGCTATATAATAATA 77
DB 245 TATCTTTTATGACACA 229

```

```

RESULT 12
US-09-925-300-816
: Sequence 816, Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben,
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05988
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 816
: LENGTH: 551
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (2)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (15)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-816

```

```

Query Match          5.6%; Score 48; DB 10; Length 551;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 60; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

```

Search completed: May 1, 2003, 23:35:10
Job time : 159.5 secs

Search completed: May 1, 2003, 23:35:10
Job time : 159.5 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

8903.503 Million cell updates/sec

Sequence: 1 ctcgagttttttttt.....gggatccactagtctaga 856

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

Database :

1:	gb_emb1.*
2:	gb_hbg.*
3:	gb_in.*
4:	gb_om.*
5:	gb_ov.*
6:	gb_pat.*
7:	gb_ph.*
8:	gb_pl.*
9:	gb_pr.*
10:	gb_ro.*
11:	gb_sts.*
12:	gb_sy.*
13:	gb_un.*
14:	gb_v1.*
15:	em_ba.*
16:	em_fun.*
17:	em_hum.*
18:	em_in.*
19:	em_mu.*
20:	em_om.*
21:	em_or.*
22:	em_ov.*
23:	em_pat.*
24:	em_ph.*
25:	em_pl.*
26:	em_ro.*
27:	em_sts.*
28:	em_un.*
29:	em_v1.*
30:	em_hbg_hum.*
31:	em_hbg_in.*
32:	em_hbg_other.*
33:	em_hbg_mu.*
34:	em_hbg_pl.*
35:	em_hbg_ro.*
36:	em_hbg_un.*
37:	em_hbg_v1.*
38:	em_sy.*
39:	em_hbg_hum.*
40:	em_hbg_mu.*
41:	em_hbg_other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	856	100.0	856	6	ARI148907	ARI148907 Sequence
2	842.4	98.4	855	6	ARI148906	ARI148906 Sequence
3	799.6	93.4	864	8	ABO27504	ABO27504 Arabidopsis
4	763.4	89.2	840	8	AY065378	AY065378 Arabidopsis
5	635.6	74.3	780	8	ABO27505	ABO27505 Arabidopsis
6	655.6	65.3	559	8	AY133813	AY133813 Arabidopsis
7	528	61.7	528	6	E38965	E38965 Method for
8	466	54.4	109560	8	F5114	AC001229 Sequence
9	465	54.3	2483	8	AF152096	AF152096 Arabidopsis
10	389.8	45.5	799	8	ABO27506	ABO27506 Arabidopsis
11	377.6	44.1	528	8	AF152907	AF152907 Arabidopsis
12	374.4	43.7	528	6	E38986	E38986 Method for
13	289.6	33.8	745	8	ABO27456	ABO27456 Citrus un
14	248.8	29.1	899	6	AX478001	AX478001 Sequence
15	248.4	29.0	847	8	ABO52943	ABO52943 Oryza sat
16	248	29.0	847	8	ABO52944	ABO52944 Oryza sat
17	239.8	28.0	1004	6	AX478049	AX478049 Sequence
18	238.6	27.9	866	6	ABO62676	ABO62676 Oryza sat
19	230.4	26.9	1191	6	AX478007	AX478007 Sequence
20	225.2	26.3	1078	6	AX477997	AX477997 Sequence
21	220.6	25.8	886	6	AX478033	AX478033 Sequence
22	196	22.9	936	6	AX478029	AX478029 Sequence
23	187	21.8	969	6	AX478027	AX478027 Sequence
24	185.8	21.7	492	6	AX477991	AX477991 Sequence
25	176.8	20.7	668	6	AE1530	AE1530 Sequence 4
26	176.8	20.7	668	6	ATU077674	U77674 Arabidopsis
27	175	20.4	837	6	AX478005	AX478005 Sequence
28	174.4	20.4	954	8	AF316419	AF316419 Lolium pe
29	171.6	20.0	950	8	AF159882	AF159882 Oryza sat
30	168.8	19.7	597	8	ABO24715	ABO24715 Arabidopsis
31	168.8	19.7	886	8	AY065211	AY065211 Arabidopsis
32	168.4	19.7	613	6	AX478043	AX478043 Sequence
33	166.8	19.5	559	8	AY096515	AY096515 Arabidopsis
34	166.4	19.4	980	6	AX478011	AX478011 Sequence
35	164	19.2	10936	8	ATF9F13	AL080253 Arabidopsis
36	164	19.2	197568	8	ATCHRI1V53	AL161523 Arabidopsis
37	160.6	18.8	577	8	AF145259	AF145259 Nicotiana
38	159.4	18.6	902	6	AX478009	AX478009 Sequence
39	159	18.6	907	8	AF159883	AF159883 Oryza sat
40	157.6	18.4	1295	6	AX478021	AX478021 Sequence
41	154.8	18.1	560	8	AF145260	AF145260 Nicotiana
42	154.4	18.0	869	8	LEU84140	U84140 Lycopersicon
43	146.8	17.1	558	8	AF145261	AF145261 Nicotiana
44	145.8	17.0	4377	8	ATU087834	U87834 Arabidopsis
45	136	15.9	354	8	AF145262	AF145262 Nicotiana

RESULT 1
AB1A8907

LOCUS	856 bp	DNA	PAT 08-AUG-2007
DEFINITION	AR148907 Sequence 3 from patent US 6225530.		

VERSION ARI148907.1 GI:15112997

SOURCE ORGANISM

Unclassified.
1 (bases 1 to 856)

AUTHORS	TITLE
Weigel, D. and Kardailsky, I.	Flowering locus <i>TF</i> and genetically modified plants having

JOURNAL Patent: US 6225530-A 3 01-MAY-2001;

FEATURES Location/Qualifiers
source 1..856
/organism="unknown"
BASE COUNT 249 a 194 c 150 g 263 t
ORIGIN

Query Match 100.0%; Score 856; DB 6; Length 856;
Best Local Similarity 100.0%; Pred. No. 7.1e-192;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 CTCGAGTTTTTTTTTTTTTTTTTATTAATATAACACTTATTCATGATTAATA 60
Db 1 CTCGAGTTTTTTTTTTTTTTTTTATTAATATAACACTTATTCATGATTAATA 60
Oy 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTTCTCCCTCATTT 120
Db 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTTCTCCCTCATTT 120
Oy 121 TTATTACACACTTATATATGAACTATATAGGATCATACACCGTTGTTACTGTATCA 180
Db 121 TTATTACACACTTATATATGAACTATATAGGATCATACACCGTTGTTACTGTATCA 180
Oy 181 TAAATGGTTATTAATTAATTAATATAGATGATGATTAATTCATCAGATATGCAATAT 240
Db 181 TAAATGGTTATTAATTAATTAATATAGATGATGATTAATTCATCAGATATGCAATAT 240
Oy 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTTCTCTCCGAGCCACTCTCCCTC 300
Db 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTTCTCTCCGAGCCACTCTCCCTC 300
Oy 301 TGACAAATGTATAGAAAACCTGCGCCACAGGGAGCGGAGATTTAGATCTCAGCAAACTCG 360
Db 301 TGACAAATGTATAGAAAACCTGCGCCACAGGGAGCGGAGATTTAGATCTCAGCAAACTCG 360
Oy 361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACAGTTTGGCTGCGCAAGCTGTGA 420
Db 361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACAGTTTGGCTGCGCAAGCTGTGA 420
Oy 421 AACAAATATAACACAGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCTATACACACA 480
Db 421 AACAAATATAACACAGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCTATACACACA 480
Oy 481 ATCTATTTGCCAAAGGTTGTCCAGTTGTAGCAGGATATCAGTCAACCAACCAATGAGAGA 540
Db 481 ATCTATTTGCCAAAGGTTGTCCAGTTGTAGCAGGATATCAGTCAACCAACCAATGAGAGA 540
Oy 541 TATTTCTCGAGGTGAGGGTGTCTAGAGACTTGAACATCGATCCACATTAACCAAAAGTA 600
Db 541 TATTTCTCGAGGTGAGGGTGTCTAGAGACTTGAACATCGATCCACATTAACCAAAAGTA 600
Oy 601 TAGAAGTTCTCGAGGTCTTCTCCACCAATCTCACTTGGCTTGTTTGAACCTGAGAA 660
Db 601 TAGAAGTTCTCGAGGTCTTCTCCACCAATCTCACTTGGCTTGTTTGAACCTGAGAA 660
Oy 661 GGCCTTAGATCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
Db 661 GGCCTTAGATCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
Oy 721 GATCTATTAAAGGATCAAGAGCTCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
Db 721 GATCTATTAAAGGATCAAGAGCTCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
Oy 781 ATATTATAGACATTTTATGATCTTGAACCAAAACCTGCTGTAATTTCTCAGCCGGGG 840
Db 781 ATATTATAGACATTTTATGATCTTGAACCAAAACCTGCTGTAATTTCTCAGCCGGGG 840
Oy 841 ATCCACTAGTTCTAGA 856
Db 841 ATCCACTAGTTCTAGA 856
```

RESULT 2
AR148906/c

LOCUS AR148906 855 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6225330.
ACCESSION AR148906
VERSION AR148906.1 GI:15112996
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 855)
AUTHORS Weigel, D. and Kardailsky, I.
TITLE Flowering locus T (FT) and genetically modified plants having
modulated flower development
JOURNAL Patent: US 6225330-A 1 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..856

BASE COUNT 263 a 151 c 193 g 248 t
ORIGIN

Query Match 98.4%; Score 842.4; DB 6; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-188;
Matches 854; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Oy 1 CTCGAGTTTTTTTTTTTTTTTTTATTAATATAACACTTATTCATGATTAATA 60
Db 855 CTCGAGTTTTTTTTTTTTTTTTTATTAATATAACACTTATTCATGATTAATA 796
Oy 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTTCTCCCTCATTT 120
Db 795 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTTCTCCCTCATTT 736
Oy 121 TTATTACACACTTATATATGAACTATATAGGATCATACACCGTTGTTACTGTATCA 180
Db 735 TTATTACACACTTATATATGAACTATATAGGATCATACACCGTTGTTACTGTATCA 676
Oy 181 TAAATGGTTATTAATTAATTAATATAGATGATGATTAATTCATCAGATATGCAATAT 240
Db 735 TTATTACACACTTATATATGAACTATATAGGATCATACACCGTTGTTACTGTATCA 676
Oy 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTTCTCCGAGCCACTCTCCCTC 300
Db 675 TAAATGGTTATTAATTAATTAATATAGATGATGATTAATTCATCAGATATGCAATAT 616
Oy 421 AACAAATATAACACAGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCTATACACACA 480
Db 615 C-ATTGGTTATTAAGGAAGAACCATCTAAAGTCTTCTCCGAGCCACTCTCCCTC 557
Oy 481 ATCTATTTGCCAAAGGTTGTCCAGTTGTAGCAGGATATCAGTCAACCAACCAATGAGAGA 540
Db 556 TGACAAATGTATAGAAAACCTGCGCCACAGGGAGCGGAGATTTAGATCTCAGCAAACTCG 497
Oy 541 TATTTCTCGAGGTGAGGGTGTCTAGAGACTTGAACATCGATCCACATTAACCAAAAGTA 600
Db 496 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACAGTTTGGCTGCGCAAGCTGTGA 437
Oy 601 TAGAAGTTCTCGAGGTCTTCTCCACCAATCTCACTTGGCTTGTTTGAACCTGAGAA 660
Db 421 AACAAATATAACACAGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCTATACACACA 480
Oy 661 GGCCTTAGATCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
Db 436 AACAAATATAACACAGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCTATACACACA 377
Oy 721 GATCTATTAAAGGATCAAGAGCTCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
Db 376 ATCTATTTGCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 317
Oy 781 ATATTATAGACATTTTATGATCTTGAACCAAAACCTGCTGTAATTTCTCAGCCGGGG 840
Db 541 TATTTCTCGAGGTGAGGGTGTCTAGAGACTTGAACATCGATCCACATTAACCAAAAGTA 257
Oy 841 ATCCACTAGTTCTAGA 856
Db 601 TAGAAGTTCTCGAGGTCTTCTCCACCAATCTCACTTGGCTTGTTTGAACCTGAGAA 660
Oy 256 TAGAAGTTCTCGAGGTCTTCTCCACCAATCTCACTTGGCTTGTTTGAACCTGAGAA 197
Oy 661 GGCCTTAGATCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
Db 196 GGCCTTAGATCCAAAGGTTGTCTAGTCACTCTCTTGGCCATAAGTAACCTTTAGAGATTT 137
Oy 721 GATCTATTAAAGGATCAAGAGCTCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
Db 721 GATCTATTAAAGGATCAAGAGCTCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
```

Db	136	GATCATATTAAGGATCAAGAAACGCTCCACAACTCTGCTTACTATATAAGAGGGCTCTT	77
Oy	761	ATATATTATAGACATCTTTGATCTTGGAACAAACCTGCTGCTGTAATCTCGACACCCGGGG	840
Db	76	ATATATTATAGACATCTTTGATCTTGGAACAAACCTGCTGCTGTAATCTCGACACCCGGGG	17
Oy	841	ATCCACTGCTCTCTAGA	856
Db	16	ATCCACTGCTCTCTAGA	1
RESULT 3			
LOCUS	AB027504/c	864 bp	mrna linear PLN 26-FEB-2000
DEFINITION	Arabisopsis thaliana FT ,FLOWERING LOCUS T) mRNA, complete cds.		
ACCESSION	AB027504		
VERSION	AB027504.1	GI:4903011	
KEYWORDS	FT.		
SOURCE	Arabisopsis thaliana (strain:landsberg er) cDNA to mRNA.		
ORGANISM	Arabisopsis thaliana		
REFERENCE	Enkaytopia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.		
TITLE	1 (sites)		
JOURNAL	2 (bases 1 to 864)		
MEDLINE	A pair of related genes with antagonistic roles in mediating		
REFERENCE	flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
DEFINITION	Flowering signals		
ACCESSION	Flowering signals		
VERSION	Flowering signals		
KEYWORDS	Flowering signals		
SOURCE	Flowering signals		
ORGANISM	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE	Flowering signals		
AUTHORS	Flowering signals		
TITLE	Flowering signals		
JOURNAL	Flowering signals		
MEDLINE	Flowering signals		
REFERENCE			

Accession	Gene	Protein	Length	Source
AY065378	LOCUS	840 bp	linear	PLN 26-APR-2002
AY065378	DEFINITION	Arabidopsis thaliana putative flowering signals mediating protein		
AY065378	ACCESSION	AY065378		
AY065378	VERSION	AY065378.1	GI:17529185	
AY065378	KEYWORDS	FLI-CDNA		
AY065378	ORGANISM	Arabidopsis thaliana		
AY065378	REFERENCE	1 (bases 1 to 840)		
AY065378	REFERENCE	Yamada, K., Iltu, S.-X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,		

to this work. Shinozaki, K. (RIKEN GSC) and rheologists, A. (SSP /PSEC) contributed equally to this work as PIs.

location/Qualifiers

1. .559

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="1"

/clone="U11796"

/note="This clone is in pUNI 51.

ecotype: Columbia"

1. .559

/gene="At1g65480"

1. .528

/gene="At1g65480"

/codon_start=1

/evidence=experimental

/product="putative flowering signals mediating protein FT"

/protein_id="AA091747.1"

/db_xref="GI:22136806"

/translation="MSINIRDPILVSRVGDVDPFNSITLKYTGQREVTGIDILR
PSQVQNPVEIGEDLRNFETLVMDPVSFNSPHLRFLHMLTDPATGTGTTG
NEIVCENPSTAGIHRVVFILFRQLGRQVYARAGWQNFRTREAEIYNGLVAV
FYNGQREGCGGRLL"

529. .559

3'UTR

BASE COUNT 151 a 117 c 132 g 159 t

ORIGIN

Query Match 65.3%; Score 559; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 AATATCAATGTTTAAAGAGAGACATCTAAAGTCTTCTCCGACGACCTCT 295
Db 559 AATATCAATGTTTAAAGAGAGACATCTAAAGTCTTCTCCGACGACCTCT 500

QY 286 CCCCTGACAAATTTAGAAAACGCGCCACGCGGAGGCGGAGATTGATCTCAGCA 355
Db 499 CCCCTGACAAATTTAGAAAACGCGCCACGCGGAGGCGGAGATTGATCTCAGCA 440

QY 356 ACTGCGAGTGTGAAGTTCTGGCGCCACCCGTGTCATACACTTTTGGCCGCAAGCT 415
Db 439 ACTGCGAGTGTGAAGTTCTGGCGCCACCCGTGTCATACACTTTTGGCCGCAAGCT 380

QY 416 GTCGAAACAATATAACACGACAGATGAATTCCTGCAATGAGGACTTGGATTTCGTAAC 475
Db 379 GTCGAAACAATATAACACGACAGATGAATTCCTGCAATGAGGACTTGGATTTCGTAAC 320

QY 476 ACACAAATCTATGCGCAAGGTTGTCAGTTGTAGCAGGATATCACTCACCAACCAAT 535
Db 319 ACACAAATCTATGCGCAAGGTTGTCAGTTGTAGCAGGATATCACTCACCAACCAAT 260

QY 536 GGAGATATTCGCGAGTGAGGAGGTTGCTAGGACTTGAACAATCTGGATTCACCATTAACA 595
Db 259 GGAGATATTCGCGAGTGAGGAGGTTGCTAGGACTTGAACAATCTGGATTCACCATTAACA 200

QY 596 AAGTATAGAGTCTCTGAGGTTCTTCACCAATCTCAACTCTTGGCTTTGTTGAACCT 655
Db 199 AAGTATAGAGTCTCTGAGGTTCTTCACCAATCTCAACTCTTGGCTTTGTTGAACCT 140

QY 656 GAGAAGGCTTGAATCCAGGATTAAGTACCTCTCTTGGCGATTAAGTAACTTAAG 715
Db 139 GAGAAGGCTTGAATCCAGGATTAAGTACCTCTCTTGGCGATTAAGTAACTTAAG 80

QY 716 TGATTGATCTATTAAGGATCAAGAGCTCTCCAAACAATCTGGTTACTATAAGAGGT 775
Db 79 TGATTGATCTATTAAGGATCAAGAGCTCTCCAAACAATCTGGTTACTATAAGAGGT 20

QY 776 CTCTTATATTTATAGACAT 794
Db 19 CTCTTATATTTATAGACAT 1

RESULT 7
E38985/c 528 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Method for shortening plant generation and plant.
ACCESSION
VERSION E38985.1 GI:18625004
KEYWORDS JP 2000139250-A/1.
SOURCE
ORGANISM Arabidopsis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae.
REFERENCE
1 (bases 1 to 528)
Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.
TITLE Method for shortening plant generation and plant
JOURNAL Patent: JP 2000139250-A 1 23-MAY-2000;
TORAY IND INC

COMMENT
OS Arabidopsis
PN JP 2000139250-A/1
PD 23-MAY-2000
PE 11-NOV-1998 JP 1998320219
PR
PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
A01H1/00, A01H5/00, C12N5/10, C12N15/09, C12N5/10, C12R1:91, PC
(C12N15/09, C12R1:91), C12N5/00, C12N15/00, (C12N5/00, C12R1:91), PC
(C12N15/00, C12R1:91)
CC
FT source 1.528 location/Qualifiers
FH key location/Qualifiers
FT source 1.528 location/Qualifiers

FEATURES
source location/Qualifiers
1. .528
/organism="Arabidopsis"
/db_xref="taxon:3701"

BASE COUNT 143 a 111 c 129 g 145 t

ORIGIN

Query Match 61.7%; Score 528; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.4e-114;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CTAAAGTCTTCTCTCCGACGACCTCTCCTCTGACAAATTTGAAAACGCGGCCAC 326
Db 528 CTAAAGTCTTCTCTCCGACGACCTCTCCTCTGACAAATTTGAAAACGCGGCCAC 469

QY 327 GGAAGGCCGAGATGTGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGCGCCACC 386
Db 468 GGAAGGCCGAGATGTGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGCGCCACC 409

QY 387 TGTGATACACTGTTTCTCTGCCAAGCTGTGAAAACAATATAACAGACAGATGAAT 446
Db 408 TGTGATACACTGTTTCTCTGCCAAGCTGTGAAAACAATATAACAGACAGATGAAT 349

QY 447 TCTGCAATGAGACTTGTGATTTCTGACACCAATCTCATTTGCCAAGTTTCTCAGT 506
Db 348 TCTGCAATGAGACTTGTGATTTCTGACACCAATCTCATTTGCCAAGTTTCTCAGT 289

QY 507 TGTACAGGATATCATGATCAACCAATGAGATATCTCGAGAGTGAAGTTCTAGG 566
Db 288 TGTACAGGATATCATGATCAACCAATGAGATATCTCGAGAGTGAAGTTCTAGG 229

QY 567 ACTTGAACATCTGATCCACCAATTAAGATTAAGATTTCTGAGTCTTCTCAGC 626
Db 228 ACTTGAACATCTGATCCACCAATTAAGATTAAGATTTCTGAGTCTTCTCAGC 169

QY 627 AATCTCACTCTTGGCTTTTGAACCTGAGAGGCTTGAATCCAGCATTAAGTAC 686
Db 168 AATCTCACTCTTGGCTTTTGAACCTGAGAGGCTTGAATCCAGCATTAAGTAC 109

QY 687 CTCTCTTGGCGATTAAGTAACTTAAGTATTAATTAAGGATCAAGAGCTC 746
Db 108 CTCTCTTGGCGATTAAGTAACTTAAGTATTAATTAAGGATCAAGAGCTC 49

GVGVSNDLILGFAKLFNDELTLTDINIRSRVNMCKYMGISPEFGDVALRYMLRKLQE
 IKKDKLIKAGVESLSSEALRQACREGRMQLQTSVEEMREQLVDMDLSTLNHSPSS
 LLISR"
 complement(47061..49870)
 /gene="F5114.8"
 complement(join(47061..47422,47541..47632,47766..47824,
 47929..48015,48122..48218,48320..48525,48704..48799,
 48884..48959,49053..49153,49242..49418,49467..49532,
 49587..49654,49750..49870))
 /gene="F5114.8"
 /note="Similar to Zea mays permease 1 (gb|U43034)."
 /codon_start=1
 /evidence=not-experimental
 /protein_id="AB60909.1"
 /db_xref="GI:2190545"
 /translation="MTNGSGGNNGAANRTELOPHPYKEQLPGIOYCVNSPPMLEAV
 VLGHVHLISGLIVLIPSMLEFFPPFFPEFLNESLIFAEKVKVOTLPLPSGLT
 TLRSFGCTRLPVAVASXAYIIPITSIYTRTYTIDPERVRRIRRSIQGALIT
 CGEVLICILCWNRNIVFLPSLAPATFTGSLTHIGPLIYNMQISFIFOLAR
 CVELGFLGLLILVTOYLPRFLMKRGVMILDSRCDRYGMILCPLWLPADLTS
 SGVLDKSHSTQTSRDRDGLINTNPWYIPYEFOMSGPFEDITDSFAMAAAEVLL
 FESTGLFYASARYSATPIPSVYVRGCMGVGLNMGITGJITSTENGSLA
 MTKIGSRVIOISAAPMIFSIPEGKGFASIPLPIMASLYCLVCPVCSFSSHI
 CSAFSTNICIFPFTKIKNSITVMAVGLSLQPCNLNSNINIKFIIIGSFPMALSTP
 OYREYVNGMRSDHSHWSTYSIL"
 complement(50678..52743)
 /gene="F5114.9"
 complement(join(50678..51059,51406..51488,51567..51733,
 51818..52033,52078..52294,52510..52743))
 /gene="F5114.9"
 /note="Strong similarity to Arabidopsis
 zeta-crystallin-like protein (gb|I49268)."
 /codon_start=1
 /evidence=not-experimental
 /protein_id="AB60917.1"
 /db_xref="GI:2190553"
 /translation="MGEYSYVENKVKILKNVDCIPETDMKYLGETIELKARKGS
 CFLVKNLISCDPIRMGRMDHFGSYLPEYPGKCEVLEFVLEIGLFEEREMC
 RCTVLALESCDPSRCDFEDWYIMLRKLELILVLFKLFEDNLSPTFVILM
 RIEGFGARVYDSDNTNPKPGDIYSGIIMBEYSLSSDMLQRLNQLDDIDPLM
 LGILMAGFTAYAGNEIICPCKDGSEVSAAGVQLVOLAKLHCGYVVGSGSK
 OKVILKNEIGYDAFNYKKEADLDLTKRYPERGIDYIPNNVCGSMADALLMKYR
 GRILCGMVSLOSSTSSQCKIKNLSAIIKRLRLEGFLOSPLIFPOLENVKRYIK
 EKVIVYEDISEGDLAPALVGLFSGNIGKQYVRAKE"
 complement(53168..54916)
 /gene="F5114.10"
 complement(join(53168..53386,53596..54114,54461..54916))
 /gene="F5114.10"
 /note="Strong similarity to Solanum polygalacturonase
 precursor (gb|U23053)."
 /codon_start=1
 /product="F5114.10"
 /protein_id="AB60920.1"
 /db_xref="GI:2190556"
 /translation="MALFLSVQVFSIVITITMSEGOFAKTSLVNLSRANNGVY
 ESAKASDAMDACGVESVIVPKGRVYLSGVREGESECKREITLRLDGLIP
 QDSYSLGKKNWSEFSGVHNVTYLGSGEDAKGSLWCKANGYNCPEATLIRMDSN
 NVKIKGVLNSQLFHAIINCRNLIKEDVNIAPDESPTNGIHLQSTDEVRMS
 IKRGDDCISIGPTGKNLMDVGTICGPGHGISLGIASIEEGVENVYKAVAVRD
 NGLRIKSMRHSNGEVRVRIGAIIMVNSPILIDNVCYCGDSSCSQEGKILNDY
 IYSGIMKTSATEIAIKMDCSEKVPCTIRMDALNLTISGEAKTSCTNVSGLGLVT

Query Match 54.4%; Score 466; DB 8; Length 109560;
 Best Local Similarity 100.0%; Pred. No. 8.3e-100;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TATAAATTAACACTTCATTCATGATAGATTAATTAATTCGATACACACTATATA 85
 |||||||
 Db 13000 TATAAATTAACACTTCATTCATGATAGATTAATTAATTCGATACACACTATATA 12941
 |||||||
 QY 86 AGTAAACACGCTCATTTCCCTCCCTCCATTTTATATACACACTATATATGAACT 145
 |||||||
 Db 12940 AGTAAACACGCTCATTTCCCTCCCTCCATTTTATATACACACTATATATGAACT 12881

QY 146 ACTATAGCATCATCACCGCTTCTACTCGTATCATTAATGTTATTAATTAATATAC 205
 |||||||
 Db 12880 ACTATAGCATCATCACCGCTTCTACTCGTATCATTAATGTTATTAATTAATATAC 12821
 |||||||
 QY 206 TATAGATGATTAATCTCATCATCAGATGATGCAATATCAATGTTATTAAGGAAGCA 265
 |||||||
 Db 12820 TATAGATGATTAATCTCATCATCAGATGATGCAATATCAATGTTATTAAGGAAGCA 12761
 |||||||
 QY 266 TCTAAGCTCTTCTCCGCGACCATCTCCCTGCAATATGTAAGAACTGGCGGCA 325
 |||||||
 Db 12760 TCTAAGCTCTTCTCCGCGACCATCTCCCTGCAATATGTAAGAACTGGCGGCA 12701
 |||||||
 QY 326 CGGGAAGCGCGAATGTTAGATCTCAGAAACTCCGAGTGTGAAGTTCGGCCACC 385
 |||||||
 Db 12700 CGGGAAGCGCGAATGTTAGATCTCAGAAACTCCGAGTGTGAAGTTCGGCCACC 12641
 |||||||
 QY 386 CTGTGTCATACCTGTTTCCCTGCGCAAGCTGTGCAACATTAACACGACGATGAA 445
 |||||||
 Db 12640 CTGTGTCATACCTGTTTCCCTGCGCAAGCTGTGCAACATTAACACGACGATGAA 12581
 |||||||
 QY 446 TTCTGCACTGAGCTTGATTTGCTTAACACACATTCATTTGCC 491
 |||||||
 Db 12580 TTCTGCACTGAGCTTGATTTGCTTAACACACATTCATTTGCC 12535
 |||||||

RESULT 9
 AF152096/c
 LOCUS 2483 bp DNA linear PLN 22-DEC-1999
 DEFINITION Arabidopsis thaliana flowering locus T (FT) gene, complete cds.
 ACCESSION AF152096
 VERSION AF152096.1 GI:6117977
 KEYWORDS
 SOURCE
 ORGANISM Arabidopsis thaliana.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; euclidyales; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2483)
 Kardalisky,I., Shukla,V.K., Ahn,J.H., Dagenais,N.,
 Christensen,S.K., Nguyen,J.T., Chory,J., Harrison,M.J. and
 Weigel,D.
 Activation tagging of the floral inducer FT
 Science 286 (5446), 1962-1965 (1999)
 MEDLINE 20050959
 PUBMED 10583961

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 2 (bases 1 to 2483)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Kardalisky,I. and Weigel,D.
 Direct Submission
 Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk
 Institute for Biological Studies, 10010 N. Torrey Pines Road, La
 Jolla, CA 92037, USA

FEATURES
 source
 location/Qualifiers
 1..2483

1..2483
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="1"
 /map="90 CM; F5114"
 1..2483
 /gene="FT"
 join(1..264,1080..1141,1855..1895,2020..2483)
 /gene="FT"
 /product="flowering locus T"
 1..63
 /gene="FT"
 join(64..264,1080..1141,1855..1895,2020..2243)
 /gene="FT"
 /function="induces flowering"
 /note="similar to hippocampal cholinergic neurostimulating
 peptide (HCNP) precursor, phosphatidylethanolamine binding
 protein (PEBP) and Raf kinase inhibitor protein;
 corresponds to Arabidopsis thaliana BAC F5114 sequence

OY 690 TCTTGGCCATAGTACCTTTAGAGTATGATCTATTAACGAGTCAAGACGCTGCC 749
 Db 136 TCTATGGCCATAGTACGATAGAGAGACCACTCGTGAAGGATCAAGAACATCTCC 77
 OY 750 AACAACTGCTACTATAGAGGCTCTCTATATTAATAGACCTTTGATCTGGAAC 808
 Db 76 AACAACTGCGAGCAGACAGAGATCTCTAGACTTAAGACATATTAATCTTGATC 18
 RESULT 11
 AF152907/c 528 bp mRNA linear PLN 22-DEC-1999
 LOCUS Arabidopsis thaliana twin sister of FT (TSF) mRNA, complete cds.
 DEFINITION AF152907
 VERSION AF152907.1 GI:6117979
 KEYWORDS
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 528)
 Kardalisky, I., Shukla, V.K., Ahn, J.H., Dagenais, N.,
 Christensen, S.K., Nguyen, J.T., Chory, J., Harrison, M.J. and
 Weigel, D.
 Activation tagging of the floral inducer FT
 Science 286 (5446), 1962-1965 (1999)
 MEDLINE 20050959
 PUBMED 10583961
 REFERENCE 2 (bases 1 to 528)
 Haakma, S., Shukla, V.K., Ahn, J.H. and Weigel, D.
 Direct Submission
 Submitted (19-MAY-1999) Plant Biology Laboratory, The Salk
 Institute for Biological Studies, 10010 N. Torrey Pines Road, La
 Jolla, CA 92037, USA
 FEATURES
 source location/Qualifiers
 1..528
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="IV"
 /map="between 93883 and g13836"
 1..528
 /gene="TSF"
 /gene="TSF"
 1..528
 /gene="TSF"
 /note="flowering locus T (FT) homolog: similar to
 hippocampal cholinergic neurostimulating peptide (HCNP)
 precursor, phosphatidylethanolamine binding protein (PEBP)
 and Raf kinase inhibitor protein"
 /codon_start=1
 /product="twin sister of FT"
 /protein_id="AA03937.1"
 /db_xref="GI:6117980"
 /translation="MSLSRDPVGVSGVDVDPFTRLVSLKTYGHHREYTGIDLR
 PSQVLPKPIVEIGDDDEPRLVMDVDPVSPSPQRETLHMLVTDIPATGNAG
 NEVVCESPRPSPGIHRIIVLVEFRLGRQTVAVAGMRQGFRTREFAEIYVGLPVAAS
 YFNCQRENGCGGRRT"
 BASE COUNT 123 a 116 c 142 g 147 t
 ORIGIN
 Query Match 44.1%; Score 377.6; DB 8; Length 528;
 Best Local Similarity 82.2%; Pred. No. 8.3e-79;
 Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
 OY 267 CTAAAGTCTTCTCCGCGACCACTCTCCCTGACAAATTGTAAGAACTCGGGCCAC 326
 Db 528 CTAGTCTCTCTCCGCGACCACTCTCCCTGACAAATTGTAAGAACTCGGGCCAC 469
 OY 327 GGGAAGCGGAGATTGATGATCTGCAAACTCGGAGTGTGAAGTTCGGCGCCACC 386
 Db 468 AGGAAGCAAGATTGATGATCTGCAAACTCGGAGTGTGAAGTTCGGCGCCACC 409

OY 387 TGGTCATACACTGTTGGCTGCCAAGCTGTGCAAAATATTAACGACGATGAT 446
 Db 408 CGGTGCATTAACCGTTTGTCTTCAGATTGCCGGAACATATACCAACAAATGATGAT 349
 OY 447 TCCCTGATGGGACTTGGATTTTCTGTAACGACATCTCATTTGCCAAGGTTGTCAGT 506
 Db 348 TCCCGAGGGGGAGCGTGGACTCTGTACGACACCACTCATTTGCCAAGGCTTCAGT 289
 OY 507 TGTACGAGGATATGATGATGACCAACCAATGAGATATTCGAGGTAGGTTGCTAGG 566
 Db 288 GGTGCGAGGTATATGATGATGACCAACCACTGAGATATTCGTTGTTAGGTTGCTAGG 229
 OY 567 ACTTGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
 Db 228 ACTCGGACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 169
 OY 627 AATCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
 Db 168 AATCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 109
 OY 687 CTCTCTTGGCCATAGTACCTTTAGAGTATGATCTATTAACGATCAAGACGTC 746
 Db 108 CTCTCTATGCGCATAGTACCTTTAGAGTATGATCTATTAACGATCAAGACATC 49
 OY 747 TCCAAACAACCTGCTTACTATAGAGGCTCTCTATATTAATATAGACAT 794
 Db 48 TCCAAACAACCTGCTTACTATAGAGGCTCTCTATATTAATATAGACAT 1
 RESULT 12
 E38986/c 528 bp DNA linear PAT 31-JAN-2002
 LOCUS E38986
 DEFINITION Method for shortening plant generation and plant.
 ACCESSION E38986
 VERSION E38986.1 GI:18625005
 KEYWORDS JP 2000139250-A/2.
 SOURCE Arabidopsids.
 ORGANISM Arabidopsids.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae.
 1 (bases 1 to 528)
 Araki, T., Kodayash, K., Ogawa, K. and Shirai, M.
 Method for shortening plant generation and plant
 Patent: JP 2000139250-A 2 23-MAY-2000;
 TORAY IND INC
 COMMENT OS Arabidopsids
 PN JP 2000139250-A/2
 PD 23-MAY-2000
 PF 11-NOV-1998 JP 1998320219
 PR
 PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
 A01H1/00, A01H5/00, C12N5/10, C12N5/09, C12N5/10, C12N1/91, PC
 (C12N15/09, C12R1/91), C12N5/00, C12N15/00, (C12N5/00, C12R1/91), PC
 (C12N15/00, C12R1/91)
 CC
 FT key location/Qualifiers
 FT source 1..528
 /organism="Arabidopsids"
 /db_xref="taxon:3701"
 BASE COUNT 122 a 117 c 142 g 147 t
 ORIGIN
 Query Match 43.7%; Score 374.4; DB 6; Length 528;
 Best Local Similarity 81.8%; Pred. No. 4.7e-78;
 Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 OY 267 CTAAAGTCTTCTCCGCGACCACTCTCCCTGACAAATTGTAAGAACTCGGGCCAC 326
 Db 528 CTAGTCTCTCTCCGCGACCACTCTCCCTGACAAATTGTAAGAACTCGGGCCAC 469

QY	327	GGGAAGGCCGAGATTGTGTGATCTAGCAAACTCCGATGTGAAGTTCCGCCCAACC	386
Db	468	AGGAAGACCAAGATTGTATGATCTCAGCAAACTCAAGATGTTGAACITTTGGCCCAACC	409
QY	387	TGTGTGATACACTGTCTTTCCTGCCAAGCTGTGAAACATATTAACACGACAGATGAAT	446
Db	408	CGGTGCATTAACCCCTTTGTCTTCGAGAGTTGCCGGACAAATACCAACAAATACGATGAAT	349
QY	447	TCCTGCAGTGGAGACTTGGATTTTGGTAAACACAAATCCATATGCCAAAGGTTCCTCAGT	506
Db	348	TCCCGAGGGGGGAGCTGTGACTCTCTGTACACACCACTCATATGCAAAAGGATTTCCAGT	289
QY	507	TGTAGCAAGGATATTCAGTCACCAACCAATGGAGATATTTCTCGAGGTGAGGGTTGCTAAG	566
Db	288	GGTGGCAGGTATATCAGTCACCAACCAAGTGGAGATATTTCTGTTGGTGAAGGTTGCTTGG	229
QY	567	ACTTGGAAACATCTGTGATCCACCATTAACCAAGTATAGAAGTTCTGTAGGTTCTTCCACC	626
Db	228	ACTGGGCACATCAGAGATCCACCATTAACCAAGGTGTAGAAATTTCTGGAAGTGTCTCCACC	169
QY	627	AATCTCAACTTWTGGCTGTTTGAACCTGGAAGGCTTGTGATTCACCAAGCATTAAGTAC	686
Db	168	AATCTCAACTTWTGGCTGTTTGAACCTGGAAGGCTTGTGATTCACCAAGCATTAAGTAC	109
QY	687	CTTCTCTTGGCCATTAAGTAACTCTTGAAGTATGATCTATTTAAACGGATCAAGACGTC	746
Db	108	CTTCTCTTGGCCATTAAGTAACTCTTGAAGTATGATCTATTTAAACGGATCAAGACGTC	49
QY	747	TCGCAACACACTGTGCTTAATAATAAGGGCTCTTATATTATTATTAACAT 794	
Db	48	TCGCAACACACTGTGCTTAATAATAAGGGCTCTTATATTATTATTAACAT 1	

FEATURES	AB027456/c	745 bp	mrna	linear	PLN 26-FEB-2000
SOURCE	AB027456				
ORGANISM	Citrus unshiu				
REFERENCE	AB027456				
AUTHORS	AB027456.1				
TITLE	CIT.				
JOURNAL	Citrus unshiu (strain: Miyagawa-wase satsuma mandarin) developing stage juice sac and pulp segment cDNA to mRNA.				
MEDLINE	Citrus unshiu				
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.				
JOURNAL	1 (sites)				
MEDLINE	Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Arai, T.				
REFERENCE	A pair of related genes with antagonistic roles in mediating flowering signals				
JOURNAL	Science 286 (3446), 1960-1962 (1999)				
MEDLINE	20050958				
REFERENCE	2 (bases 1 to 745)				
JOURNAL	Omura, M., Kobayashi, Y. and Arai, T.				
FEATURES	Submitted (17-MAY-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu, Shimizu, Shizuoka 424-0292, Japan (E-mail: om330@okt.affrc.go.jp, Tel: 81-543-69-7108, Fax: 81-543-69-2115)				
SOURCE	Location/Qualifiers				
	1..745				

gene	1. 745
CDS	/gene="ClFT" 96. 629 /gene="ClFT" /note="extensive homology to FT (FLOWERING LOCUS T

AB027504)	and TSF (TWIN SISTER OF FT, AB027506) genes of Arabidopsis thaliana
	similar to mammalian phosphatidylinethanolamine binding protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"
	/codon_start=1
	/protein_id="BA77836.1"
	/db_xref="GI:4903139"
	/translation="MSSRERKDPILVGVAVGDVLDNFTPTIPMRITYSNKDQVNGREIKPSEVLNQPRAEILGGDILRTETVLLVMWDADSPSDPSLRLELHLVLDIPATTCASGQOEIVNYESPRPTGIRHFRVFLVFLQLRQTVAYAGCGMQRNSTRDFAELVNLGPPVAAVYFNCORESGSGGGRVRR"
BASE COUNT	195 a 150 c 180 g 220 t
ORIGIN	
Query Match	33.8%; Score 289.6; DB: 8; Length 745;
Best Local Similarity	72.3%; Pred. No. 5,1e-58;
Matches 376;	Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY	277	CTTCTCCGCGAGCAGCTCTCCCTCTGCACAATTTGTGAAGAACTGCGGCGACGGGAAGGCG	336
Db	613	CTTCGCGCGGATCCGCTCTCCCTCTGGGACGTTGAAGTAGACAGCGGCGCACGGAGGTC	554
QY	337	AGATTGTGATGTCACGCAAACTCGCGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATAC	396
Db	553	AGATTGTAAACCTCAGCAAAAATCCCTCGTGTGAAGTTCTCAGCGCCACCCTGGTGCATAA	494
QY	397	ACTGTTTCCGCGCAAGCTGTGCAAAACAAATATAAACAGCAACGATGGAATTCCTGCAGTG	456
Db	493	ACAGTCTCCCTCCCAAGTTGGCGGACACAAACAAAGCAACCTGTGAATCCCATCGTT	434
QY	457	GGACTTGGATTTTGGTAAACACAAATCTCATTTGCCAAAGTGTGTCAGTTGTAGCAGG	516
Db	433	GGCCTAGGGGCTTTTATATGTTCAATCTCTGGGCCAAAGCTGGGCCCTGTGTGTCGTA	374
QY	517	ATATCAGTCACCAACCAATGGAGATATTCGTGGAGGTGAGGTTGCTAGGATCGTAGACA	576
Db	373	ATATCAGTCACCAACCAATGCAATATCTCCTTAAGGCTGGGGTACTTGGGCTTGGTGA	314
QY	577	TCTGGATCCACCATTAACCAAAAGTATAGAATTCTCGAGGCTCTTCCACCAATCTCAACT	636
Db	313	TCAGAGTATCAACCAATTAACCAAGTATTAATAATGCTCTTAAGATCATCCACCAATTTCAACC	254
QY	637	CTTGGCTGTTTGAACCTGGAAGGCGCTTGGATCCAGGCCATTTGATGTAACCTCTGTTGG	696
Db	253	CTAGGCTGGTTCAAGACTTCCAGAAAGTTTGAAGCTCAGCGCCATTATTAACATCTTGTGTT	194
QY	697	CCATTAAGTAACTTTAGAGTAGATGATCTATTTAAACGGATCAGAAAGCTGTCCAAACAAT	756
Db	193	GAATGTGAATTCATTCATTTGAATGTTCTGTGAAATAATGTCAAGAAACATCAACCAACAG	134
QY	757	CTGCTTACTATAAGAGGCTCTTATATTTATTTATAGACACT	796
Db	133	CGGCCCAATTAAGAGATCTCTCTCCCTGTGCATAT	94

[illegible]

c	10	176	20.6	792	24	ABK82093	Novel floral meristem encoding novel
c	11	176	20.6	792	24	ABK82091	Novel floral meristem encoding novel
c	12	176	20.6	792	24	ABK82092	Novel floral meristem encoding novel
c	13	176	20.6	1225	24	ABK82122	Novel floral meristem encoding novel
c	14	175	20.4	787	24	ABK82094	Novel floral meristem encoding novel
c	15	161.2	18.8	519	22	AAC90668	Strawberry flowerlet Arabidopsis pathogen
c	16	145.8	17.0	4512	19	AAV66749	Arabidopsis pathogen Anthrithum centro
c	17	116	13.6	929	18	AAAT60139	Anthrithum centro
c	18	82.6	9.6	3696	22	AAC90666	Strawberry flowerlet Arabidopsis termin
c	19	80	9.3	1330	18	AAAT60142	Strawberry flowerlet Arabidopsis termin
c	20	71.8	8.4	822	12	AAO14832	OV-16 antigen. On Strawberry flowerlet
c	21	63	7.4	4952	22	AAC90667	Human ovarian anti-Spinach lycopene e
c	22	55.6	6.5	567	24	ABO55599	Porcine complement hBovine embryonic g
c	23	52.8	6.2	2426	22	AAD17465	Bovine embryonic g Human colon cancer
c	24	51.8	6.1	1637	20	AAZ30973	Proliferative gloom Proliferative gloom
c	25	51.2	6.0	970	24	ABN73995	Human meta
c	26	51	6.0	988	24	ABN74181	Human meta
c	27	50.2	5.9	557	22	AAH35052	Human meta
c	28	50.2	5.9	18585	24	ABL34609	Human meta
c	29	50	5.8	649	22	AAK60828	Human meta
c	30	49.2	5.7	503	23	ABK41982	CDNA encoding nove
c	31	49.2	5.7	925	25	ABN74030	Bovine embryonic g
c	32	49.2	5.7	978	22	ABA77091	Proliferative gloom
c	33	49.2	5.7	83391	24	ABO67094	Human angiogenesis
c	34	49	5.7	1012	22	ABA77106	Proliferative gloom
c	35	48.8	5.7	956	24	ABN74279	Bovine embryonic g
c	36	48.8	5.7	2637	24	AAD34120	Human secreted prot
c	37	48.6	5.7	427	24	AEQ34500	Human ovarian, anti-DNA transcrip
c	38	48.6	5.7	475	22	AAK62481	Human immune/hae
c	39	48.4	5.7	7589	24	ABK28390	Novel CDNA encodin
c	40	48.2	5.6	367	22	AAZ28106	Bovine embryonic g
c	41	48.2	5.6	939	24	ABN73081	Human prostate can
c	42	48	5.6	551	21	AAE16381	Human colon cancer
c	43	48	5.6	654	22	AAH34361	Bovine embryonic g
c	44	48	5.6	910	24	ABN73980	Bovine embryonic g
c	45	48	5.6	910	24	ABN73981	Bovine embryonic g

XX WPI: 1999-611305/52.
DR P-PDSB; AAY9098.
XX
FT New flowering locus T polypeptide that regulates flowering time,
PT particularly used to accelerate flowering -
PS
XX Claim 5; Fig 2; 64pp; English.
XX
CC This sequence is the flowering locus T (FT) gene of *Arabidopsis thaliana*.
CC FT regulates flowering in plants by modulating flowering time.
CC Overexpression of FT results in early flowering, while loss of function
CC mutations or antisense directed to FT causes late flowering. The FT
CC polypeptide has a molecular weight of approximately 20kd, and is located
CC on chromosome 1. The FT polypeptide is used in the invention to modulate
CC flowering time in many mono and di-cotyledonous plants. The FT
CC polynucleotide sequence is used for recombinant production of the
CC polypeptide, and as a source of antisense, ribozyme or triplex forming
CC sequences. The FT polypeptide can also be used to raise antibodies and to
CC screen for modulators or cellular binding proteins. The methods of the
CC invention allow for the production of crops at any time of year.
XX
XQ Sequence 856 BP; 263 A; 150 C; 194 G; 249 T; 0 other;

Query Match	100.0%	Score 856;	DB 20;	Length 856;
Best Local Similarity	100.0%	Pred. No. 3.8e-190;		
Matches 856; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY		1	CTCGAGTGTGTTTTTTTTTTTTTTTTTTATTAATAATTAACACTTCATTGCATGTGATTAATA	60
Dd		856	CTCGAGTGTGTTTTTTTTTTTTTTTTTTATTAATAATTAACACTTCATTGCATGTGATTAATA	797
OY		61	TAAATTATGCATCACACACTATATAAGTAAAACTCTCATTTTCTCCCTCCTCATTT	120
Dd		796	TAAATTATGCATCACACACTATATAAGTAAAACTCTCATTTTCTCCCTCCTCATTT	737
OY		121	TTATTACCACTTATATATGTAAGTACATATGGCATCATACCCTTGCTACTCGATACA	180
Dd		736	TTATTACCACTTATATATGTAAGTACATATGGCATCATACCCTTGCTACTCGATACA	677
OY		181	TAAAATGGTTATTTAATAATTAATAACTATAGATGCATAAATCTCATTCAGATATGCATAT	240
Dd		676	TAAAATGGTTATTTAATAATTAATAACTATAGATGCATAAATCTCATTCAGATATGCATAT	617
OY		241	CAATTGGTTATTAAGAAGAAAGCCATTAAGTCTTCTTCCGCCAGCACTCTCCCTC	300
Dd		616	CAATTGGTTATTAAGAAGAAAGCCATTAAGTCTTCTTCCGCCAGCACTCTCCCTC	557
OY		301	TGACAAATTGTAGAAAACTCGCGGCCACGGGAAGGCCGGAATTTTAAATATCAGACCAAATCG	360
Dd		556	TGACAAATTGTAGAAAACTCGCGGCCACGGGAAGGCCGGAATTTTAAATATCAGACCAAATCG	497
OY		361	CGAGTGTGAAGTCTGCGGCCACCCCTGCTGATACACTGTTTGGCTGCCAAGCTGTGCA	420
Dd		496	CGAGTGTGAAGTCTGCGGCCACCCCTGCTGATACACTGTTTGGCTGCCAAGCTGTGCA	437
OY		421	AACCATATTAACACAGACACGATGAATTCCTGAGAGGGGACTGGATTTTGGTAAACACACA	480
Dd		436	AACCATATTAACACAGACACGATGAATTCCTGAGAGGGGACTGGATTTTGGTAAACACACA	377
OY		481	ATTCATATGCCAAAGGTTGTTCCAGTTTATAGCAGGGAATATCAGTACCAACCAATGGAGA	540
Dd		376	ATTCATATGCCAAAGGTTGTTCCAGTTTATAGCAGGGAATATCAGTACCAACCAATGGAGA	317
OY		541	TATTTCTCGAGAGTAGGGTTGCTAGGACTTGGAACATCTGGATCCACCATTAACCAAAAGTA	600
Dd		316	TATTTCTCGAGAGTAGGGTTGCTAGGACTTGGAACATCTGGATCCACCATTAACCAAAAGTA	257
OY		601	TAGAAAGTTCCTGAGAGTCTTCTCCACCAATCTCAACTCTGGCTTTGTTGAACCTGAGAGA	660
Dd		256	TAGAAAGTTCCTGAGAGTCTTCTCCACCAATCTCAACTCTGGCTTTGTTGAACCTGAGAGA	197
OY		661	GGCCTTAGATCAACCAACCATTAAGTACACTCTCTTTGGCCATTAAGTAACCTTTAAGATGATT	720

Db	196	GGCCTTAGATCCAAGCCATTAGTACCTCTCTTTGGCCATTAAGTAACCTTTAGAGTATT	137
Qy	721	GATCTATTAAACGGATCAAGAACCTCTCCAAACATCTGCTTACTATAAAGGGTCTCTT	780
Db	136	GATCTATTAAACGGATCAAGAACCTCTCCAAACATCTGCTTACTATAAAGGGTCTCTT	77
Qy	781	ATATTATTAGACATCTTTGATCTTTGAACAACAACCTCGTGTGAATTCCTGCAGCCCGGGG	840
Db	76	ATATTATTAGACATCTTTGATCTTTGAACAACAACCTCGTGTGAATTCCTGCAGCCCGGGG	17
Qy	841	ATCCACTAGTCTCTAGA	856
Db	16	ATCCACTAGTCTCTAGA 1	

RESULT 2
AAZ28491
ID AAZ28491 standard; cDNA; 856 BP.

AC AAZ28491;

DT 17-JAN-2000 (first entry)

DE Flowering locus T (FT) gene antisense insert.

KM Flowering locus T gene; FT; flowering time; modulator; early flowering;
KN antibody; cellular binding protein; crop; antisense construct; ss.

OS *Arabidopsis thaliana*.

PN W09953070-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08151.

PR 15-APR-1998; 98US-0060726.

PA (SALK) SALK INST BIOLOGICAL STUDIES.
YYPI Weigel D;
yy

DR WPI; 1999-611305/52.

PT New flowering locus 1 polypeptide that regulates flowering time, particularly used to accelerate flowering -

XX Example 2: E1a 3: 6400: Enc11eb
PS

This is the flowering locus T (FT) gene antisense polynucleotide sequence. This sequence is used in the production of the antisense construct of the invention pSK1060. FT regulates flowering in plants by modulating flowering time. Overexpression of FT results in early flowering, while loss of function mutations or antisense directed to FT causes late flowering. The FT polypeptide has a molecular weight of approximately 20kD, and is located on chromosome 1. The FT polypeptide is used in the invention to modulate flowering time in many mono and di-cotyledonous plants. The FT polynucleotide sequence is used for recombinant production of the polypeptide, and as a source of antisense, ribozyme or triplex forming sequences. The FT polypeptide can also be used to raise antibodies and to screen for modulators or cellular binding proteins. The methods of the invention allow for the production of crops at any time of year.

Sequence 856 BP; 249 A; 194 C; 150 G; 263 T; 0 other;

Query Match	100.08;	Score 856;	DB 20;	Length 856;
-------------	---------	------------	--------	-------------

```
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

1 CTCGAGTTTTTTTTTTTTTTTAAATATATAACACCTTCATTTCATGATTAATA 60
 |||||
 |||||

Db 1 CTCGAGTTTTTTTTTTTTTTTTTAAATATACACTTCATTTGATGATTAATA 60
QY 61 TAAATATCGCATCAGACATATATAGTAAACCTCTCATTTTCCCTCCCTCATTT 120
Db 61 TAAATATCGCATCAGACATATATAGTAAACCTCTCATTTTCCCTCCCTCATTT 120
QY 121 TTATTACACACTTTATATTGAACTACTATAGGATCATATCCGTTGGTTAGTATCA 180
Db 121 TTATTACACACTTTATATTGAACTACTATAGGATCATATCCGTTGGTTAGTATCA 180
QY 181 TAAATGTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 181 TAAATGTTATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 CAATGTTTAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 300
Db 241 CAATGTTTAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 300
QY 301 TGACAAATTTAGAAATTCGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGACAAATTTAGAAATTCGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 CGAGTGTGAAGTTCTGCGCCAGCCTGCTGATACATCTGTTCTGCGCAAGCTGCGA 420
Db 361 CGAGTGTGAAGTTCTGCGCCAGCCTGCTGATACATCTGTTCTGCGCAAGCTGCGA 420
QY 421 AACATTTAAACAGACAGATGATTTCTGCACTGGAGCTTGATTTTGTAAACACA 480
Db 421 AACATTTAAACAGACAGATGATTTCTGCACTGGAGCTTGATTTTGTAAACACA 480
QY 481 ATCTCATTTGCCAAAGTTGTTCCAGTTGTGACAGGAGATGATGACCAACCAATGGGA 540
Db 481 ATCTCATTTGCCAAAGTTGTTCCAGTTGTGACAGGAGATGATGACCAACCAATGGGA 540
QY 541 TATTTCTGAGGTGAGGTTGCTAGAGCTTGAACATCTGGATCCACCATTAACCAAGTA 600
Db 541 TATTTCTGAGGTGAGGTTGCTAGAGCTTGAACATCTGGATCCACCATTAACCAAGTA 600
QY 601 TAGAGTTCTGAGGTTCTTCCACCAATCTCAACTCTGGCTGTTTGAACCTGAGAA 660
Db 601 TAGAGTTCTGAGGTTCTTCCACCAATCTCAACTCTGGCTGTTTGAACCTGAGAA 660
QY 661 GGCCTTATGATCAAGCATTAAGTACCTCTTTGGCATTAAGTACCTTTAGAGTAT 720
Db 661 GGCCTTATGATCAAGCATTAAGTACCTCTTTGGCATTAAGTACCTTTAGAGTAT 720
QY 721 GATCTATTAACGGATCAAGACGTCCTCAACACTGCTTACTATTAAGAGGTCCTT 780
Db 721 GATCTATTAACGGATCAAGACGTCCTCAACACTGCTTACTATTAAGAGGTCCTT 780
QY 781 ATATTTATAGACATCTTTGATCTTTGAACAAACCTGCTGTAATTCCTGACGCCGGGG 840
Db 781 ATATTTATAGACATCTTTGATCTTTGAACAAACCTGCTGTAATTCCTGACGCCGGGG 840
QY 841 ATCCACTAGTTCTAGA 856
Db 841 ATCCACTAGTTCTAGA 856

RESULT 3
ID ANC34682 standard; DNA: 775 BP.

AC AAC34682;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7506.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127452.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0148175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150864.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
Best Local Similarity 99.9%; Pred. No. 5.3e-152;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 119 TTTTATTACACTTATATATATGACTACTATAGCATCATCACCCTTGTACTCTGAT 178
DB 758 TTTTATTACACTTATATATATGACTACTATAGCATCATCACCCTTGTACTCTGAT 699
QY 179 CATTAATGCTTATTAATTAATTAATCTATAGTCATTAATCTCATGAGTATGCAAT 238
DB 698 CATTAATGCTTATTAATTAATTAATCTATAGTCATTAATCTCATGAGTATGCAAT 639
QY 239 ATCAATGCTTATTAAGGAAGAGCCATCTAAAGTCTTCTCCGCGAGCCATCTCC 298
DB 638 ATCAATGCTTATTAAGGAAGAGCCATCTAAAGTCTTCTCCGCGAGCCATCTCC 579
QY 299 TCTGCAATTTGTAAGAAATGCGGCCGCGGAGGCGGAGATTTGATCTCAGCAAACT 358
DB 578 TCTGCAATTTGTAAGAAATGCGGCCGCGGAGGCGGAGATTTGATCTCAGCAAACT 519
QY 359 CCGAGCTTTGAAGTCTCGGCCGACCCGTCGTCATACCTGTTTCCCGCAAGCTGTC 418
DB 518 CCGAGCTTTGAAGTCTCGGCCGACCCGTCGTCATACCTGTTTCCCGCAAGCTGTC 459
QY 419 GAACATATTAACACGACGACGATGATCTCGACGTGGAGCTTGATTTGTAACACA 478
DB 458 GAACATATTAACACGACGACGATGATCTCGACGTGGAGCTTGATTTGTAACACA 399
QY 479 CAATCTCATTCGCAAGGTTGTCAGTTGACAGGATATCAGTACCAACCAATGGA 538
DB 479 CAATCTCATTCGCAAGGTTGTCAGTTGACAGGATATCAGTACCAACCAATGGA 538

Db 398 CAATCTCATTCGCCAAGGTTGCTCAGTTGTAGCAGGGATATCATGCAACCAACCAATGCA 339
QY 539 GAAATTCCTCGAGGTGAGGGTTGCTAGACTTGAAATCATGATCCACCATTAACCAAG 598
Db 338 GATATTTCTCGAGGTGAGGGTTGCTAGACTTGAAATCATGATCCACCATTAACCAAG 279
QY 599 TATAGAGTTCCCTGAGGTTCTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAG 658
Db 278 TATAGAGTTCCCTGAGGTTCTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAG 219
QY 659 AAGGCTTATGATCCAGCCATTAATCACTCTTTGGCCATTAAGTAACCTTTAGAGTGA 718
Db 218 AAGGCTTATGATCCAGCCATTAATCACTCTTTGGCCATTAAGTAACCTTTAGAGTGA 159
QY 719 TTGATCTATTAAGGATCCAGGATCTCCACCAACTCTCTTACTTATAGAGGCTCTC 778
Db 158 TTGATCTATTAAGGATCCAGGATCTCCACCAACTCTCTTACTTATAGAGGCTCTC 99
QY 779 TTATATTTATGACATCTTTGATCTTGACAAAC 812
Db 98 TTATATTTATGACATCTTTGATCTTGACAAAC 65
RESULT 4
AAC48359/c
ID AAC48359 standard; DNA: 754 BP.
AC AAC48359;
DX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130440.
PR 23-APR-1999; 9905-0130510.
PR 23-APR-1999; 9905-0130891.
PR 28-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 06-MAY-1999; 9905-0132487.
PR 07-MAY-1999; 9905-0132863.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.

PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 14-JUN-1999; 9905-0138847.
PR 16-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 21-JUN-1999; 9905-0139763.
PR 22-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.

PR 28-JUL-1999; 990S-0145951.
 PR 02-AUG-1999; 990S-0146386.
 PR 02-AUG-1999; 990S-0146388.
 PR 02-AUG-1999; 990S-0146389.
 PR 03-AUG-1999; 990S-0147038.
 PR 04-AUG-1999; 990S-0147204.
 PR 04-AUG-1999; 990S-0147302.
 PR 05-AUG-1999; 990S-0147192.
 PR 05-AUG-1999; 990S-0147260.
 PR 06-AUG-1999; 990S-0147303.
 PR 06-AUG-1999; 990S-0147416.
 PR 09-AUG-1999; 990S-0147493.
 PR 09-AUG-1999; 990S-0147935.
 PR 10-AUG-1999; 990S-0148171.
 PR 11-AUG-1999; 990S-0148319.
 PR 12-AUG-1999; 990S-0148341.
 PR 13-AUG-1999; 990S-0148565.
 PR 13-AUG-1999; 990S-0148684.
 PR 16-AUG-1999; 990S-0149368.
 PR 17-AUG-1999; 990S-0149175.
 PR 18-AUG-1999; 990S-0149426.
 PR 20-AUG-1999; 990S-0149722.
 PR 20-AUG-1999; 990S-0149723.
 PR 20-AUG-1999; 990S-0149929.
 PR 23-AUG-1999; 990S-0149902.
 PR 23-AUG-1999; 990S-0149930.
 PR 25-AUG-1999; 990S-0150566.
 PR 26-AUG-1999; 990S-0150884.
 PR 27-AUG-1999; 990S-0151065.
 PR 27-AUG-1999; 990S-0151066.
 PR 27-AUG-1999; 990S-0151080.
 PR 30-AUG-1999; 990S-0151303.
 PR 31-AUG-1999; 990S-0151438.
 PR 01-SEP-1999; 990S-0151930.
 PR 07-SEP-1999; 990S-0152363.
 PR 10-SEP-1999; 990S-0153070.
 PR 13-SEP-1999; 990S-0153758.
 PR 15-SEP-1999; 990S-0154018.
 PR 16-SEP-1999; 990S-0154039.
 PR 20-SEP-1999; 990S-0154779.
 PR 22-SEP-1999; 990S-0155139.
 PR 23-SEP-1999; 990S-0155486.
 PR 24-SEP-1999; 990S-0155659.
 PR 28-SEP-1999; 990S-0156458.
 PR 29-SEP-1999; 990S-0156596.
 PR 04-OCT-1999; 990S-0157117.
 PR 05-OCT-1999; 990S-0157753.
 PR 06-OCT-1999; 990S-0157865.
 PR 07-OCT-1999; 990S-0158025.
 PR 08-OCT-1999; 990S-0158232.
 PR 12-OCT-1999; 990S-0158369.
 PR 13-OCT-1999; 990S-0159293.
 PR 13-OCT-1999; 990S-0159294.
 PR 13-OCT-1999; 990S-0159295.
 PR 13-OCT-1999; 990S-0159329.
 PR 14-OCT-1999; 990S-0159330.
 PR 14-OCT-1999; 990S-0159331.
 PR 14-OCT-1999; 990S-0159637.
 PR 14-OCT-1999; 990S-0159638.
 PR 18-OCT-1999; 990S-0159584.
 PR 21-OCT-1999; 990S-0160741.
 PR 21-OCT-1999; 990S-0160767.
 PR 21-OCT-1999; 990S-0160768.
 PR 21-OCT-1999; 990S-0160770.
 PR 21-OCT-1999; 990S-0160814.
 PR 21-OCT-1999; 990S-0160815.
 PR 22-OCT-1999; 990S-0160980.
 PR 22-OCT-1999; 990S-0160981.
 PR 22-OCT-1999; 990S-0160989.
 PR 25-OCT-1999; 990S-0161404.
 PR 25-OCT-1999; 990S-0161405.
 PR 25-OCT-1999; 990S-0161406.
 PR 26-OCT-1999; 990S-0161359.

PR 26-OCT-1999; 990S-0161360.
 PR 26-OCT-1999; 990S-0161361.
 PR 28-OCT-1999; 990S-0161920.
 PR 28-OCT-1999; 990S-0161992.
 PR 28-OCT-1999; 990S-0161993.
 PR 29-OCT-1999; 990S-0162142.

Query Match 80.8%; Score 692; DB 21; Length 754;
 Best Local Similarity 100.0%; Pred. No. 6,5e-152;
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 TTATTACACTTATATATGTAAGTCTATAGGCATCACCAGTCTTACTCGATCA 180
 |||||||
 DB 754 TTATTACACTTATATATGTAAGTCTATAGGCATCACCAGTCTTACTCGATCA 695
 QY 181 TAAATGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 |||||||
 DB 694 TAAATGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 635
 QY 241 CAATTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
 |||||||
 DB 634 CAATTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 575
 QY 301 TGACATTTGTAAGAACTGCGCCAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 |||||||
 DB 574 TGACATTTGTAAGAACTGCGCCAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 515
 QY 361 CGAGTTGTAAGTTGCGGGCCACCCTGGTGCATACACTGTTGCTGCGCAAGCTGCGA 420
 |||||||
 DB 514 CGAGTTGTAAGTTGCGGGCCACCCTGGTGCATACACTGTTGCTGCGCAAGCTGCGA 455
 QY 421 AACCAATTAAGACGACGACGATGAATTCCTGCAAGTGGACTGGATTTTGGTAACACA 480
 |||||||
 DB 454 AACCAATTAAGACGACGACGATGAATTCCTGCAAGTGGACTGGATTTTGGTAACACA 395
 QY 481 ATCTCATTTGCCAAGTTGTTCCAGTTGTAGCAGGATATCACTGATCCCAACCAATGAGA 540
 |||||||
 DB 394 ATCTCATTTGCCAAGTTGTTCCAGTTGTAGCAGGATATCACTGATCCCAACCAATGAGA 335
 QY 541 TATCTCGAGGAGTGGAGTGTGAGGACTTGGAACTGATCCCAACCAATGAGA 600
 |||||||
 DB 334 TATCTCGAGGAGTGGAGTGTGAGGACTTGGAACTGATCCCAACCAATGAGA 275
 QY 601 TAGAAGTCTCTGAGTCTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAGA 660
 |||||||
 DB 274 TAGAAGTCTCTGAGTCTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAGA 215
 QY 661 GGCCTTAGATCCAGCATTTAGTCACTCTCTTTGGCCATAGTAACCTTTAGAGTGATT 720
 |||||||
 DB 214 GGCCTTAGATCCAGCATTTAGTCACTCTCTTTGGCCATAGTAACCTTTAGAGTGATT 155
 QY 721 GATCTATTAAAGGATCAAGAGTCTCCCAACACTGCTTACTTAAAGAGGCTCTT 780
 |||||||
 DB 154 GATCTATTAAAGGATCAAGAGTCTCCCAACACTGCTTACTTAAAGAGGCTCTT 95
 QY 781 ATATTATTAGACATCTTGTGATCTGAACAAC 812
 |||||||
 DB 94 ATATTATTAGACATCTTGTGATCTGAACAAC 63

RESULT 5
 AAA60683/c
 ID AAA60683 standard; DNA; 528 BP.
 XX
 AC AAA60683;
 XX
 DT 26-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.
 XX
 KW Arabidopsis thaliana; Cruciferae; plant; control; flowering;
 solar radiation; ds.
 XX

QY	447	TCCTGCAGTGGGACTTGGATTTTCGTAAACACAATCTCAATGCGCAAGGTTGTCCAGT	506
Db	348	TCCCGAGGGGGAGCTGGAGCTCTGTGACACACCCTCAATTGCCAAGGCATTTCACGT	289
QY	507	TGTAGCAGGGATATACGTACACCAACCAATGAGATATCTCGGAGGTGAGGGTTGCTAGG	566
Db	288	GGTGGCAGGTATATACGTACACCAACCAGTGGAGATATCTGTGTGGAGAGGTTGCTTGG	229
QY	567	ACTTGGAAACATCTGGATGCCACCATTAACCAAGTATTAAGTCTCGTGGATCTCTCCACC	626
Db	228	ACTGGGCACATCTGGATGCCACCATTAACCAAGTATTAAGTCTCGTGGATCTCTCCACC	169
QY	627	AATCTCAACTCTTGGCTTTGTTTGAACCTGAGAGGCCCTTAGATCCAAAGCCATTAGTCAC	686
Db	168	AATCTCAACTTATGTTTGTTCACAACTTGAGAGGCCCTTAGATCCAAAGCCATTAGTCAC	109
QY	687	CTCTCTTTGGCCATTAACATAACCTTAAGATGATCTATTAACCGATCAAGAACGTC	746
Db	108	CTCTCTATATGGCCATTAAGTAGACCTTAAGAGAGAACCACTGTGAAGAGATCAAGAACATC	49
QY	747	TCGCAACAACCTGCTTACTATTAAGAGGCTCTCTATATTTATAGACAT	794
Db	48	TCGCAACAACCTGCTGAGCACCAAGAGATCTCTAAGCATTAAGACAT	1

RESULT 7
AAA60684/c
ID AAA60684 standard; DNA; 528 BP

DT	26-OCT-2000 (first entry)
----	---------------------------

DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.

KM Arabidopsis thaliana; Cruciferae; plant; control; flowering
KM solar radiation; ds.

OS *Arabidopsis thaliana*.

PN JP20000139250-A

PD 23-MAY-2000.

PF 11-NOV-1998; 98JP-0320219

PR 11-NOV-1998; 98JP-0320219

PA (TORA) TORAY IND INC.

DR WPI: 2000-425906/37.

PT A method to accelerate plant generation and generation accelerated

1
XX
XX

CC the present invention describes a method to accelerate plant generative
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
CC of the present invention.

SQ Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;

Query Match	43.7%	Score 374.4	DB 21	Length 528
Best Local Similarly	81.8%	pred.No. 6.9e-78		
Matches 432; Conservative	0;	Mismatches 96;	Indels 0;	Gaps 0;

QY	267	CTAAGCTCTCTCCCGGACGACCTCCCTGTGACATTTGTAGAAATCTGGCCAC	326
Db	528	CTACGTTCTTTTCCCCACAGCCATTCTCCCTCTGGCACTTAAGTAAAGACACCCAC	469
QY	327	GGGAGGCCGAGATTGTAGATCTCAGCAAACTCGCGAGTTGTAGTTCTGGGCCACCC	386
Db	468	AGGAAGACCAAGATTGTATGATCTCAGCAAACTCCGAGTGTGTAAGTGTGGGCCACCC	409
QY	387	TGTGTGCTATCACTTTTGGCTTCCCAACCTGTCCAAACAATATAACGACAGATGAAT	446
Db	408	CGGTGCATAAACCGTTTGCTCTCCGAGTTGCCGGAACAATAACCAACAATACGATGAAT	349
QY	447	TCTCGCAGTGGAGTTGTGGATTTTCGTACACACATCTCAATCCGCAAGGTTTGTCAGT	506
Db	348	TCCCGAGGGGGGAGTGGAGTCTGTGTACACACACCTCATTTGCCAAAGCAATTCACAT	289
QY	507	TGTAGCAGGATATCACTCACCAACCAATGAGATATTTCTCGAGGTGAGAGTTGCTAGG	566
Db	288	GGTGGCAGGTATATCAGTACACCAACCGTGAAGATTTCTGTGTGGAGGGTGTGCTTGG	229
QY	567	ACTTGAACATCTGTGATCCACCATTAACCAAGTATAGAGTTCTCGAGTCTCTCCAC	626
Db	228	ACTCGGCAGCATCAGGATCCACCATTAACCAAGTATAGAAATTTCTGAAGTCGTCTCTCC	169
QY	627	AATCTCAACTTTGGCTTTGTTTAACCTGGAAGGCTTAGATCCAAAGCATTTAGTCAC	686
Db	168	AATCTCACTATTGGTTGTTCACAACTTAGAAGGCTTAGATCCAAAGCATTTAGTAAC	109
QY	687	CTCTCTTTGGCATTAAGTAACCTTTTAGTAGTATGATCTATTAAACGATCAAGAAGTC	746
Db	108	CTCTCTATGGCATTAAGTAGACCTTAAGAGAGACCAACTGTGAAAGGATCAAGAACATC	49
QY	747	TCCAACAACCTCTGCTTACTATTAAGAGGCTCTTATATTTAATAGACAT	794
Db	48	TCCAACAACACTGCCGACCAAGAGAGATCTCTCGACTTAAGACAT	1

RESULT 8
AAC90636/c
ID AAC90636 standard; cDNA; 522 BP.

AC AAC90636;

DT 20-MAR-2001 (first entry)

DE	Strawberry flowering regulation protein coding sequence	SEQ ID NO: 5

KW Strawberry; flowering regulation; floral homeotic gene; field crop;

KW harvesting; fruit production; ss.

OS *Fragaria vesca*.

PN WO200071722-A1.

PD 30-NOV-2000.

PF 24-MAY-2000; 2000WO-US14297.

PR 25-MAY-1999; 99US-0318789.

XX

XX

XX

DR P-PSDB; AAB50266.

PT Novel nucleic acid involved in controlling plant flowering processes is

PT plants having altered flowering behavior such as early, delayed or day-neutral flowering -

CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles.

XX
 XX Sequence 762 BP; 188 A; 178 C; 176 G; 220 T; 0 other;

Query Match 20.6%; Score 176; DB 24; Length 762;
 Best Local Similarity 60.0%; Pred. No. 1.4e-31;
 Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1

QY	260	AAGCATCTAAAGTCTTCTCTCCGACGCCACTCTCCCTGACAAATGTAAGAAAC	319
Db	622	AAGAACTCGATTCTTCGAGCCCTCCGACGACGTCTCTCTGACAAATGGAAGTAAC	563
QY	320	CGGCGACGGGAAGGCCGAGATGTGAGATCTGACAAACTCGGAGAGTTGAAGTTCTGGC	379
Db	562	CAGCCACAGGGAGGCCAAGATCATTTATCCACAGCAAACTGGGGGTGTGAATATATCC	503
QY	380	GCCACCCCTGGTGACATACACTGTTTCCCTGCCAAGCTGTGCGAAACATATATAACACGAC	439
Db	502	TGAAGGAAGGACACATATACAGTCTCCCTTCGCTTGGAAGACACAAAATGTAAC	443
QY	440	GATGAATCTCTGACAGTGGACCTTGATATTTTGGTAACACAAATCTCATTTGCCAAGTTG	499
Db	442	TGTGATATCCAAATGTTGGGCTTTGGGCTCTCATACTCATGTGACCTCCGCCAAATGAAG	383
QY	500	TTCAGTGTGAGAGGATATTCAGTACACCAACCAATGGAGATATTCGCGAGGTGAGGAT	559
Db	382	CATCTGTGTCCCAAGTATATTACTGACATATCCAGTGAAGATGCTCCGCAATATACGAT	323
QY	560	TGTTAGGACTTGGAGAACATCTGGATCCACCATTAACCAAAAGTATAGAAGTCTTGAGGCTT	619
Db	322	CACTTGGTCTGAGCACAATCTGGGTCCGCATTAACCAATGTGAATTAAGATCCGAACTAC	263
QY	620	CTCCACCAATCTCAACTCTTGGCTTGTGTAACCTGAGAGGCGCTTGAATCCAAAGCAT	679
Db	262	CCCCCTGAACCTCTACTCTTGGTTAGATATACAACTGATGGGTAGAGCTCATGACAT	203
QY	680	TATGTACC---TCTCTTTGGCCATTAAGTAACTTTAGAGTGAATGATCTATTAACGGAT	736
Db	202	TGAAGACCAAGCTGTTGTTAGTATATAGGTTGTCATACCATCTTCAACATATGGTTAAAGAT	143
QY	737	CAAGAACTCTCCACAACTCTGCTAGCTATGAAGGGCTC	776
Db	142	CGAGAACTTCTCCAAATGACACGACCAACATATGAAGGCTC	103

RESULT 11
 ABR82091/c
 ID ABR82091 standard; cDNA: 792 BP.
 XX ABR82091;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA encoding novel floral meristem identity protein lpcEna.
 XX
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;
 KW CEN; CEN-like protein; APERIAL2; AP2; AP2-like protein; HB;
 KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing; male sterility;
 KW biomass increase; branching increase; blocking flowering;

KW allergenic pollen; floral meristem identity protein; gene; ss.
 XX *Lolium perenne*.
 XX WO200233091-A1.
 XX 25-APR-2002.
 XX 17-OCT-2001; 2001WO-AU01311.
 XX 19-OCT-2000; 2000AU-0000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI: 2002-452388/48.
 XX P-PSDB: ABG60933.
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX Claim 4; Fig 30; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box
 CC gene activities may alter flower, embryo and seed development, e.g.,
 CC enhance or inhibit embryo differentiation and growth or alter flower
 CC organ identity through conversion of one floral organ in another.
 CC Manipulation of CEN or HB activity in plants alters the control of phase
 CC change, flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles.
 XX
 CC Sequence 792 BP; 196 A; 181 C; 181 G; 232 T; 2 other.
 XX
 QY Query Match 20.6%; Score 176; DB 24; Length 792;
 Db Best Local Similarity 60.0%; Pred. No. 1,4e-31;
 Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;
 QY 260 AAGCATTCTAAGCTCTCTCCGCGACGACCTCCCTGCAATTTAGAAAAGTG 319
 Db 625 AAGAACTGATTTTCAGGCGCTCTGCGAGGAGCTCTCTGCAATTTAGAAAAG 566
 QY 320 CGGCCAGGGAAGCGGATTTAGATCTCAGCAAACTCGAGTGTGAAGTTCTGCG 379
 Db 565 CAGCCACAGGAGGCGCAAGATCATTCACAGCAAACTGCGGGGTGTGAATGATGCC 506
 QY 380 GCCACCTGTGTACACTGTGCTGCGCAAGCTGTGCAAAATATAAACAGACAC 439

Db 505 TGAAGGAAGGACAGATACAGTCTGCCCTTCTGCTTGAAGAGCACAAAATGAACC 446
 QY 440 GATGAATTCCTGCACTGGGACTTGGATTTCGTAACACACATCTCATGGCAAAAGTG 499
 Db 445 TGTGGATTTCCAAATGTTGGGCTTGGGCTCTCATAGCTCATACCTCCCCCAATGAAG 386
 QY 500 TTCCAGTTGTAGCAGGATATCAGTACCAACCAATGAGATATTCGAGGTGAGGT 559
 Db 385 CATCTGTTGTCCACAGTATATTACTGACAAATCCAGTGAAGATGCTCCCGCAGATACGAT 326
 QY 560 TGTAGAGACTTGAACATCTGATTCACCATTAACCAAGATATGAAGTTCTGAGTCTT 619
 Db 325 CACTTGTGCTCGGACATCTGGGTCGCCCATTAACCAATGAAATAGAGATGCGAAATGATC 266
 QY 620 CTCACCAATCTCAACCTTGGCTGTGTTGAACCTGGAAGGCGCTTATGATCAACGAT 679
 Db 265 CCCCCTGAACCTTCACTCTGTTAGATTAACACACTGATGATGATGATGATGAT 206
 QY 680 TAGTCACG---TCTCTTGGCCATTAAGTAACTTGAAGTATTAAGATTAAGCGAT 736
 Db 205 TGAAGACAGCTGTGTTAGATTATAGTGTGCTTACCATTTACACATGCGTTAATGAT 146
 QY 737 CAAGAAGCTTCCAAACAATCTGCTTACTATTAAGAGGCTC 776
 Db 145 CGAGAACTTCTCAATGACACGACCAACAAATTAAGAGGCTC 106
 RESULT 12
 ABR82092/c
 ID ABR82092 standard; cDNA: 792 BP.
 XX
 XX ABR82092;
 XX
 DE 27-AUG-2002 (first entry)
 DE
 XX Novel floral meristem identity gene LpCENa contig #1.
 XX
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;
 KW CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
 KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
 KW Inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX
 OS *Lolium perenne*.
 XX WO200233091-A1.
 XX 25-APR-2002.
 XX 17-OCT-2001; 2001WO-AU01311.
 XX 19-OCT-2000; 2000AU-0000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI: 2002-452388/48.
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX Claim 4; Fig 32; 290pp; English.
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as

XX Sequence 1225 BP; 388 A; 249 C; 258 G; 330 T; 0 other;

Query Match	20.6%	Score 176; DB 24;	length 1225;
Best Local Similarity	60.0%	Pred. No. 1.6e-31;	
Matches 312; Conservative	0;	Mismatches 205;	Indels 3; Gaps 1;

Qy	260	AAGCACTTAAAGCTCTTCTCTCCGAGCAGCTCTCCCTGTGCAATTTAGAAAATG	319
Db	672	AAGAACTCGATTTTTCACGGCCTCCTGGCAGCAGCTCTCTCTGCAATTTAAGTAAACAG	6133
Qy	320	CGGCCACGGGAAGGCCAGATTTAGATCTCAGCAAACTCGCAGTGTGAAGTTCTGGC	379
Db	612	CAGCAGCAGGGAGGCCAAGATCATATTACACAGCAAACTGGCGGGTCTTTAAATGATCCC	5533
Qy	380	GCCACCCGTGGTGCATPACAGTGTGGCTGCCCAAGCTGTCCAAACATATATAACGCGAC	439
Db	552	TGAAGGAAGGCACAGATACAGTCTGCTTGGCTTCTGTCTGMAAGCACAATAATGACC	4393
Qy	440	GATGAATTCCTGCAGTGGGACTTGGATTTTGGTAAACACACAAATCTCATTCGCCAAAGTTG	499
Db	492	TGTGATATTCCAATGTGTGGGCTTGGGCTCATAGCTCAGACCTCCCCCAATGAAG	4333
Qy	500	TTCCAGTTAGTACGGGATATACATCAACCAACAAATGAGATATATTCGGAGGGTGGGT	559
Db	432	CATCTGTGTGCCAGATATATTAATGACAAATCCAGTAAAGATGCTCCCGCAGATACGAT	3737
Qy	560	TGCTAGSACTTGGAAACATCTGGATCCACATTAACCAAAAGTATAGAACTTCTGAGTCTT	619
Db	372	CACCTGGTCTCGGCACATCTGGGTCGCCCAATACCAATGTGAATTAAGATCGCAAGTCAC	3131
Qy	620	CTCCACCAATCTCAACCTTGGGGTGTGTTTGAACCTGAGAAAGCCTTAGATCCAGCAT	679
Db	312	CCCCCTAACCCTTACTCTTGGTTTAGATACAACTGCTGATGGGTAGAGCTCATGACCAT	2533
Qy	680	TAGTCACC---TCTCTTTGGCCATTAAGTAAACCTTTAGAGTGAATGATCTTTTAAACGAT	736
Db	252	TGAAGACCACTTGTGTGAGTATTAAGTGTCTCAACATCTTCACACATAGGTTTAATGAT	1533
Qy	737	CAGAAGCTGCCAACAACCTGCTTACTATTAAGAGGTC	776
Db	192	CGAGAACTTCTCCATGACGACGACCAACAATTAAGAGGCTC	153

RESULT 14
ABK82094/c
ID ABK82094 standard; cDNA; 787 BP.

XX	ABK82094;	
AC		
XX		
DT	27-AUG-2002	(first entry)
XX		
DE	Novel floral meristem identity gene LpCENa contig #3	

KM *PCG:RAG1;fescuse*: MAOS-box; MADS: MADS-like protein; CENTRORADIALIS;
KM *CEN-1-like protein*: APTAL2A; AP2; AP2-like protein; HB;
KM *Homo-box protein*: HB-like protein; plant growth; plant architecture;
KM *Inflorescence development*: flower development; embryo development;
KM *seed development*: flower organ identity; phase change; male sterility
KM *hybrid seed production*: herbage quality; early maturing crop;
KM *blomass increase*; branching increase; blocking flowering;
KM *allergenic pollen*; floral meristem identity protein; ss.

OS Lolium perenne.

PN WO200233091-A1

PD 25-APR-2002.

PF 17-OCT-2001; 2001WO-AU01311.

PR 19-OCT-2000; 2000AU-0000873.

PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.

PI Spangenberg G, Sawbridge TJ, Ong EK, Emmerling M;
XX
DR WPI; 2002-452388/48.

PT New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APTPLA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases -

PS Claim 3; Fig 32; 290pp; English

CC The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-1-like
CC proteins, ADELINAE2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box
CC gene activities may alter flower, embryo and seed development, e.g.,
CC enhance or inhibit embryo differentiation and growth or alter flower
CC organ identity through conversion of one floral organ in another.
CC Manipulation of CEN or HB activity in plants alters the control of phase
CC change, flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production
CC increasing branching to enhanced biomass in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles.

Sequence 787 BP; 194 A; 180 C; 179 G; 228 T; 6 other;

Query Match	20.4%	Score 175;	DB 21;	Length 787;
Best Local Similarity	59.8%	Pred. No. 2.4e-31;		
Matches 311; Conservative	0;	Mismatches 206;	Indels 3;	Gaps 1;

QY	260	AAGCACTCTAAAGCTCTTCTTCCTCCGAGCAGCATCTCCCTGTGACATTTGTAGAAAATG	31.9
	625	AAGAACTCGATTTTCAGCGCCCTCTGGCAGCAGCTCTCTCTGCATTTGAAGTAAACAG	56.66
Db	320	CGCGCACGGGAAGGCCGAGATTGTAGATCTCAGCAAACTGCGAGTGTGAAGTTCTGGC	37.9
QY	565	CAGCCACAGGAGGCCAAAGATCATTTATCCAGCAAACTGCGGGGTGTGAATGATCCC	50.66
Db	380	GCCACCTCGTGCACTACACTGTTTGCTGCCAAGCTTCGAAACATATATAACAGCAC	43.9
QY	505	TGAAGGAAGGCACGATACAGTCTGCGCTTGCTTTCCTGAAGAGCAGCAAAAATGAAAC	44.6
Db	440	GATGAATTCCTCGAGTGGGAGCTGGATTTTCGTAAACACACATCAATCTCCAAAGTTG	49.99
QY	445	TGTGGATTTCCAAATGTTGGCGCTTGTGGCTCTCATATAGCTACAGACCTCCCGCCCAATATAG	38.66
Db	500	TTCACGTTGTAGCAGGGATATCAGTCACCAACCAATGAGATATTTCTCGAGGTTGAGGGT	55.99
QY	385	CATCTGTGTGCCAGGTATATTACTGACAAATTCAGTAGAGATGOTCCCGCAGATATCGGAT	32.66
Db	560	TGCTAGACCTTGGACATCTTGATCCACCACTTAACCAAGTATAGAACTTCTGAAGTCTT	61.9

Db 325 CACTGGTCCTGGACATCTGGTCCGCAATTAACCAATGTGAATAGGATCGAAGTCAC 266
 QY 620 CTCACCAATCTCAACTCTGGCTGTGTTGAACCTGAGAGGCTTAGATCCAGCCAT 679
 Db 265 CCCCCTGAACTCTACTCTGGTTAGATACACTGCTGATGGGTAGAGCTCATGACCAT 206
 QY 680 TACTGACCC--TCCTTGGCCATTAAGTAACCTTTAGATGATGATCTATTAAAGGAT 736
 Db 205 TGAAGACACACTGTGTTGAATATAGGTGCTACACATCTTCACACATGGGTTAATGAT 146
 QY 737 CAAGAAGCTCTCAACAACCTCTGCTTACTATTAAGAGGTC 776
 Db 145 CGAAGACTCTCCATGACACAGACCAACATTAAGAGGCTC 106

RESULT 15
 AAC90668/c
 ID AAC90668 standard; cDNA; 519 BP.

AC AAC90668;
 AC AAC90668;
 DT 20-MAR-2001 (first entry)
 DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
 XX
 KM Strawberry; flowering regulation; floral homeotic gene; field crop;
 XX harvesting; fruit production; ss.
 OS
 OS Fragaria vesca.
 PN MO200071722-A1.
 XX 30-NOV-2000.
 PD
 XX 24-MAY-2000; 2000MO-US14297.
 PF
 XX 25-MAY-1999; 99US-0318789.
 PR 24-MAY-2000; 2000US-0318789.
 XX
 PA (DMP) DNA PLANT TECHNOLOGY CORP.
 XX
 PI Oeller P, Guttererson N;
 DR MPI; 2001-025165/03.
 DR P-PSDB; AAB50271.
 XX
 PT Novel nucleic acid involved in controlling plant flowering processes is
 PT useful for generating transgenic plants, in particular strawberry
 PT plants having altered flowering behavior such as early, delayed or
 PT day-neutral flowering
 XX
 PS Claim 23; Page 94-95; 97pp; English.
 CC The present invention provides the nucleic acid and protein sequences of
 CC a number of proteins from the strawberry which are involved in the
 CC regulation of flowering. These were identified using primers based on the
 CC homologous sequences from A. thaliana, B. napus and R. sativus. They can
 CC be used in the production of transgenic field crops whose flowering is
 CC regulated and the time of fruiting and harvesting can be manipulated.
 XX
 SQ Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;

Query Match 18.8%; Score 161.2; DB 22; Length 519;
 Best-Local Similarity 57.3%; Pred. No. 3.6e-28;
 Matches 292; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 277 CTTCTCCGAGCAGCCTCTCCCTGTGACATTTGAGAAACCTGGCCAGCGAAGGCCG 336
 Db 515 CGCTCTCTCTGCTGCGCTTCTCTCTGTGATGAGTAACGCGACAGACAGAACCA 456
 QY 337 AGATTGTAGATCTGACGAACCTGCGAGTGTGAAGTTGCGGCCACCTGTGTCATAC 396
 Db 455 AGGTCTGTTTCGGCTGCGAAGGTTCGGGTGTGAAGTATCCCTTGAGGAAGCGCGGTTTC 396

QY 397 ACTGTTTGCCCTGCCAAGCTGTGCAAAACATATTAACACAGACAGATGAATTCCTGCAATG 456
 Db 395 ACCGACGTGCTTCTGTTTGTATGAGAGAACACAAACCTGTGATGCTTATGT 336
 QY 457 GGAATGGAATTTTGTAAACACACAAATTCATTTGCCAAAGTTGTCCAGTTGTAGCAGGG 516
 Db 335 GGCTTTGGCATCTGTAGCTCACCACCTCTCTTCCAAATGTAGATCTGTGTCCAGGA 276
 QY 517 ATATAGTCAACCAACAAATGAGATATTCGAGGTGAGGGTTCATAGACCTTGAAACA 576
 Db 275 ATGTCTGTACAAATCCAGTGCAGGTGCTCTTCAAAATAGGATCACTAGGGCCAGAAACA 216
 QY 577 TCTGGATCCACCAATTAACCAAGATATAGAGTTCTGTAGGCTTCCACCAATCTCACT 636
 Db 215 TCTGGTCTGTGATTAACCAAGATATGATGCTGCTCTTCAAAATAGGATCACTAGGGCCAGAAACA 216
 QY 637 CTTGGCTTGTGTTTGAACCTGAGAGGCTTGTAGATCCAAAGCATTAGTACACCTCTTTGG 696
 Db 155 CTAGTTTGGGGGTGACTGCAGAAAGGAAGGACATGCTCATGTGCAGACGCTTGTCTG 96
 QY 697 CCATTAAGTAACCTTTAAGTGTATGATCTAATTAACGAGATCAGAACGCTTCAACAAC 756
 Db 95 TTGTAAGAGACAAATCTTTTGTAGTGGGGGTGAAGGAATCAAGAACATCTCTATGACT 36
 QY 757 CTGCTTACTAATAGAGGGTCTCTTAATTT 786
 Db 35 CTTCAACAGCTAGAGGTTCCGACATTTCT 6

Search completed: May 2, 2003, 10:45:34
 Job time : 286.5 secs


```

/obj_xref="taxon:3702"
/clone="SQ183b01.F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

```

Query Match	60.3%	Score 516.4	DB 10	Length 518
Best Local Similarity	99.8%	Pred. No. 1.9e-79		
Matches 517	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	88	TAAAACTCTCATTTTCTCCCTCTCATTTTATTATACACTATATATTGAAGTAC	147
Db	61	TAAAACTCTCATTTTCTCCCTCTCATTTTATTATACACTATATATTGAAGTAC	120
QY	148	TATAGGCATATACACCGTGTGTCTGCTGATCATAAATGGATTATTAATTAATAACTA	207
Db	121	TATAGGCATATACACCGTGTGTCTGCTGATCATAAATGGATTATTAATTAATAACTA	180
QY	208	TAGATGCATAAATCTCATCATCAGAGTATGCAATATGCAATTTGGTTATTAAGAAAGAACCATC	267
Db	181	TAGATGCATAAATCTCATCATCAGAGTATGCAATATGCAATTTGGTTATTAAGAAAGAACCATC	240
QY	268	TAAAGTCTTTCCTCCGCGACACACTCCCTCTGACAATTTGTGAAAACATCGCGGCCACG	327
Db	241	TAAAGTCTTTCCTCCGCGACACACTCCCTCTGACAATTTGTGAAAACATCGCGGCCACG	300
QY	328	GGAAGCGCGAGATTGTAGATCTCAGCAAACTCGCGAGTTTGAAGTCTTGCGGCCACCT	387
Db	301	GGAAGCGCGAGATTGTAGATCTCAGCAAACTCGCGAGTTTGAAGTCTTGCGGCCACCT	360
QY	388	GSTGCATCATCTGTTTGGCTCCGACAGCTGTCGAAAACAATTAACACGACACGATGAAAT	447
Db	361	GSTGCATCATCTGTTTGGCTCCGACAGCTGTCGAAAACAATTAACACGACACGATGAAAT	420
QY	448	CTTGCAGTGGAGCTTGGATTTTGTGTAACACACAATTCATTTGCCAAAGTTGTTCAGTT	507
Db	421	CTTGCAGTGGAGCTTGGATTTTGTGTAACACACAATTCATTTGCCAAAGTTGTTCAGTT	480
QY	508	GTAGACGGATATCATGTCACCAACCAATGGATGGAATATTC	545
Db	481	GTAGACGGATATCATGTCACCAACCAATGGATGGAATATTC	518

RESULT 2	494 bp	mRNA	linear	EST 07-SEP-2000
AV562377				
LOCUS				
DEFINITION	Arabidopsis thaliana green siliques Columbia			
	thaliana cDNA clone SQ169B07F 3', mRNA sequence.			
ACCESSION	AV562377			

VERSION	AV562377.1	GI:8733803
KEYWORDS	EST.	
SOURCE	thale cress,	
ORGANISM	Arabidopsis thaliana	

REFERENCE AUTHORS TITLE
1 (bases 1 to 494) Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. A large scale analysis of cDNA in <i>Arabidopsis thaliana</i> : Generation

JOURNAL
MEDLINE
COMMENT
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

```

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asemitu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
1. 494

```

```

/tissue_type="green siliques"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

```

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
57.7%; Score 494; DB 10; Length 494;	100.0%; Pred. NO. 1.4e-75;	0;	0;	0;	0;	0
Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
29	AAATATAACACTTCATTTTCATGTAGATTAAATTAATTAATGCGATCAGACACTATATAAGT	88				
1	AAATATAACACTTCATTTTCATGTAGATTAAATTAATTAATGCGATCAGACACTATATAAGT	60				
89	AAACACCTCTCATTTTCTCCCTCCCTCATTTTATATACACCTATATATGAACTACT	148				
61	AAAAACCTCTCATTTTCTCCCTCCCTCATTTTATATACACCTATATATGAACTACT	120				
149	ATAGGCATCATCACCGTTCGTTACTCGTATCATATAAATGGTATTAAATTAATTAATTAAT	208				
121	ATAGGCATCATCACCGTTCGTTACTCGTATCATATAAATGGTATTAAATTAATTAATTAAT	180				
209	AGATGCATTAATCTCTCATCTAGAGTATGCAATATCAATTGGTTATTAAGGAAGGCACTCT	268				
181	AGATGCATTAATCTCTCATCTAGAGTATGCAATATCAATTGGTTATTAAGGAAGGCACTCT	240				
269	AAAGCTCTTCCTCCCGAGCCACTCTCCCTTGACAATTTGAGAAAATCGGGCCACGG	328				
241	AAAGCTCTTCCTCCCGAGCCACTCTCCCTTGACAATTTGAGAAAATCGGGCCACGG	300				
329	GAAGCCGAGATTGTAGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGGCCACCTCG	388				
301	GAAGCCGAGATTGTAGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGGCCACCTCG	360				
389	GTGCATATACAGTTTGCCCTGGCCAACTCTGCAAACTTAATTAACAGCAGCATGAATTC	448				
361	GTGCATATACAGTTTGCCCTGGCCAACTCTGCAAACTTAATTAACAGCAGCATGAATTC	420				
449	CTGCAGTGGAGCTTGATTTTCTGTAACACACAATCTCATTTGCCAAAGTTGTTCAGTTG	508				
421	CTGCAGTGGAGCTTGATTTTCTGTAACACACAATCTCATTTGCCAAAGTTGTTCAGTTG	480				
509	TAGCAGGGATATCA	522				
481	TAGCAGGGATATCA	494				

RESULT 3	LOCUS	423 bp	mRNA	linear	EST 28-MAR-2001
AV788551	AV788551	Arabidopsis thaliana	CDNA clone	RAFL06-80-B19 3'	

KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
1 (bases 1 to 423)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.

TITLE and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rcc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SalI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Location/Qualifiers
1..423
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF06-80-B19"
/clone.lib="RAF06"
/dev_stage="plants at various developmental stages from germination to mature seeds"
/note="Site-1: SstI; Site-2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT 131 a 99 c 70 g 123 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 423; DB 10; Length 423;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GATTAAATATATATGTCATCACACCTATATAGTAAACACTCTTCCTCCGCC 112
1 GATTAAATATATATGTCATCACACCTATATAGTAAACACTCTTCCTCCGCC 60
113 TCCATTTTATACACCTATATATAGTAAACACTCTTCCTCCGCC 172
61 TCTCATTTTATACACCTATATATAGTAAACACTCTTCCTCCGCC 120
173 TCGTATCATTAATGTTTATTAATTAATCTATAGTAAATCTCATCAGAGTA 232
121 TCGTATCATTAATGTTTATTAATTAATCTATAGTAAATCTCATCAGAGTA 180
233 TCGAATATCAATGTTTATTAATTAATGTTTATTAATCTCATCAGAGTA 292
181 TCGAATATCAATGTTTATTAATTAATGTTTATTAATCTCATCAGAGTA 240
293 TCGCCTCTGACAAATGTTTATTAATTAATGTTTATTAATCTCATCAGAGTA 352
241 TCGCCTCTGACAAATGTTTATTAATTAATGTTTATTAATCTCATCAGAGTA 300
353 CAACACTGCGAGTGTGAAGTTCTGGCGCCACCTGTCATACAGCTTGGCTGCAA 412
301 CAACACTGCGAGTGTGAAGTTCTGGCGCCACCTGTCATACAGCTTGGCTGCAA 360
413 GCTGTGAAACAATATTAACACGACGATGATTCCTGACGTGGAGCTTGGTTCGT 472
361 GCTGTGAAACAATATTAACACGACGATGATTCCTGACGTGGAGCTTGGTTCGT 420
473 AAC 475
421 AAC 423

RESULT 4
BE590867/c 551 bp mRNA linear EST 18-AUG-2000
LOCUS BE590867
DEFINITION WHE0855_C01_E012s Wheat 20-45 DAP spike cDNA library Triticum aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
ACCESSION BE590867

VERSION BE590867.1 GI:9845940
KEYWORDS EST
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
JOURNAL unpublished (2000)

COMMENT

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES

Location/Qualifiers
1..551
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0855_C01_E01"
/clone.lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site-1: EcoRI; Site-2: XhoI; Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the T7 Close Lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)

BASE COUNT 106 a 171 c 168 g 106 t
ORIGIN

Query Match
Best Local Similarity 68.9%; Score 234; DB 10; Length 551;
Matches 321; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

314 AAACCTGGCCGACGGAAGCCGAGATGTAGATCTGACGAACCTCCGAGTGTGAAGT 373
550 AGACGGCGGCGACGAGCGGCGGAGGTGTAGACCTGCGGAAGTCCGTGTTGAAGT 491
374 TCTGGCCGACCCCTGGTGATACACTGTTTCCCTGCCAAGCTGCGAACAATTAACA 433
490 TCTGGCCGACCCGCGGAGCGCTACACGCTGCGCGGAGCTGTGGAAGCGACGACA 431
434 CGACAGCATGAATCCCTGCGAGTGGGACTTGATTTGTAACACATCTCATTTGCCAA 493
430 CGAAGCATGATGATCCCATGCTCGACGAGAGGCTCTGTGACATCACTCTGCGCGA 371
494 AGGTTGTTCCAGTTGTAGACAGGATATACGACCAACATGAGATATCTCGAGGT 553
370 AGGATGACACAGTGTGACCGGGATATCTGCACAACGATGAGATATCTCCTAAGT 311
554 GAGGTTGCTAGACCTTGGAACATCTGATCCACATTAACCAAGTATAGAGTTCTCTGA 613
310 TGGGATGCTGTGACCTTGGAACATCTGATCCACATTAACCAAGTATAGAGTTCTCTGA 251
614 GGTCTTCCACCATCTCAACCTGCTGTTTGAACCTGAGAGGCTTAGATCA 673

Db 250 TCTCATTCGCCGCCACCTCACCTTGGGCTGCTGGCCGACATGAGACGGCTTGACCTGC 191

Qy 674 AGCCATTAGTACCTCTCTTGGCCATAGTAACCTTTAGATGATTTGATTAATTAACG 733

Db 190 AGCCCTTGAGACGGCTCTGTTCCGGAAGTACACCTGAGTGTGGTGGCCGATGAAG 131

Qy 734 GATCAGAACGCTCTCCAACTCTGCTTACTATAAGAGGCTCTCT 779

Db 130 GGTCCAGCAGCTGCCACACCTTGCACACACGAGGCTCTCT 85

RESULT 5
B0797327 659 bp mRNA linear EST 30-JUL-2002
LOCUS B0797327
DEFINITION B0797327 Ripening Grape berries Lambda Zap II Library Vitis
vitis cDNA clone RT071D11 3', mRNA sequence.
ACCESSION B0797327
VERSION B0797327.1 GI:22012293
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
REFERENCE 1 (bases 1 to 659)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Coulure, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Romieu C.
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
Seq primer: 77.
FEATURES
SOURCE Location/Qualifiers
1..659
/organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="RT071D11"
/cclone_1bp="Ripening grape berries Lambda Zap II Library"
/dev_stage="ripening stage"
/note="Organ: Fruit; Vector: Lambda Zap II; Site: 1: Eco RI
; Site: 2: XhoI; Oriented library construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"

BASE COUNT 197 a 155 c 124 g 183 t

ORIGIN

Query Match 27.1%; Score 231.6; DB 14; Length 659;
Best Local Similarity 74.6%; Pred. No. 1.5e-30;
Matches 291; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 268 TAAAGTCTCTCTCCGCGACGACCTGCTGACATTTAGAAACATCGCGCCGCG 327

Db 270 TATATCTTCGACACCGGACCGCCCTCTTGGCGATTAAATAAACGACGACACA 329

Qy 328 GGAAGCGGAGATTGATGATCTCAGCAAACTCGGAGTGTGAAGTCTGCGCACCT 387

Db 330 GCGAACAACAGATTATAAGCTGAGCAAAAGTCCCTAGTGTGAATTTTGGCGCACCT 389

Qy 388 GGTGCAATCACTGTTGGCTGCGCAAGCTGTGGAACAATATATAACAGACAGATGATT 447

Db 390 GGTGCAATCACTGTTGGCTGCGCAAGCTGTGGAACAATATATAACAGACAGATGATT 449

Qy 448 CTGCAATGGGACTTTCGATTTTCTAACAACAATTCATTTGCCAAAGTTTTCACATT 507

Db 450 CCAGCTGTTGGGCGGCTCTCATACACAACTCTTGGCCGAAAGTTGCCACAGA 509

Qy 508 GTAGAGGATATCATGATCACCACCAACGATATTTCCGAGGAGGCTGTAGTA 567

Db 510 GTTGTGGAAATATCAGTACCAACCAATGATAGTCTCTTGAAGTGTGAGTACTG 569

Qy 568 CTTGGAACATCTGATTCACCAATTAACCAAGATATGAAAGTCTGAGTCTTCCACCA 627

Db 570 CTGGAGCGTCAAGGGCTCCACCATTAACCAAGATATGAAAGTCTTCAAGTATCCCTTCA 629

Qy 628 ATCTCAACTCTTGCTTTGTTGAACCTGA 657

Db 630 ATGTCACCCCTTAAGTTGGCTGACTAGCTGA 659

RESULT 6
AV560420 206 bp mRNA linear EST 07-SEP-2000
LOCUS AV560420
DEFINITION AV560420 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ134d05F 3', mRNA sequence.
ACCESSION AV560420
VERSION AV560420.1 GI:8731846
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 206)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
JOURNAL MEDLINE
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
SOURCE Location/Qualifiers
1..206
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ134d05F"
/cclone_1bp="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site: 1: EcoRI; Site: 2:
XhoI"

BASE COUNT 69 a 43 c 28 g 66 t

ORIGIN

Query Match 24.1%; Score 206; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-26;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 TTTTATATACACTTATATATTTGACTATGAGTACATCAACCGTCTTACTGCTA 177

Db 1 TTTTATATACACTTATATATTTGACTATGAGTACATCAACCGTCTTACTGCTA 60

Qy 178 TCATTAATATGTTTAAATTAATTAATATAGATGATTAATATCATACAGATGCAA 237

Db 61 TCATTAATATGTTTAAATTAATTAATATAGATGATTAATATCATACAGATGCAA 120

Qy 238 TATCAATTTGTTAAAGAAAGAACCATTAAGTCTTCTTCTCGGACCACTCTCC 297

Db 121 TATCAATTTGTTAAAGAAAGAACCATTAAGTCTTCTTCTCGGACCACTCTCC 180

Qy 298 CTGCAATTTGTTAAAGAAAGAACCATTAAGTCTTCTTCTCGGACCACTCTCC 323

Db 181 CTGCAATTTGTTAAAGAAAGAACCATTAAGTCTTCTTCTCGGACCACTCTCC 206

```

RESULT 7
AY11549/c
LOCUS      AY11549      1168 bp      mRNA      linear      HTC 26-MAY-2002
DEFINITION Zea mays CL846_1 mRNA sequence.
ACCESSION  AY11549
VERSION     AY11549.1  GI:21216139
KEYWORDS
SOURCE      Zea mays.
ORGANISM    Zea mays.
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
             clade; Panicoidae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1168)
AUTHORS     Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
             Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE       Maize Mapping Project/Dupont Consensus Sequences for Design of
             Overgo Probes
JOURNAL     Unpublished (2002)
REFERENCE   2 (bases 1 to 1168)
AUTHORS     Coe,E.C.
TITLE       Direct Submission
JOURNAL     Submitted (25-APR-2002) Maize Mapping Project, University of
             Missouri, Columbia, MO 65211, USA
FEATURES
SOURCE
             1. 1168
               /organism="Zea mays"
               /db_xref="maizedb:632948"
               /db_xref="taxon:4577"
               /clone="CL846.1"
               /clone_lib="Maize Mapping Project/Dupont Consensus
               Library"
               /note="this sequence is part of a project of EST
               assemblies resulting from the application of public
               configs to seed Dupont contigs; this resource was
               assembled by Dupont as part of a collaboration for the
               overgo addressing of BACS in conjunction with the Maize
               Mapping Project"
BASE COUNT  161 a      247 c      245 g      159 t      336 others
ORIGIN
Query Match      23.3%; Score 199.4; DB 11; Length 1168;
Best Local Similarity 48.4%; Pred. No. 3.8e-25;
Matches 302; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
QY 156 TCATACCGCTTCGTACTCGTATCATTAATGTTATTAATAATTAATCTAGATGCA 215
    ||| ||| ||| ||| |||
DB 813 TCGTAATGTTGAGTAGTTGACGATCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 754
QY 216 TAAATCTATCAGAGTATGCAATATCAATGTGTTATTAAGAAGAACCATTAAGTCT 275
    ||
DB 753 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCT 694
QY 276 TCTTCCTCCGACGCACTCTCCCTGACAAATTGTAGAAAACCTGGCGCCAGGGAAGGCC 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 693 CCTGNNNNNAGAGCCGCGCTCAGCTGGAGTTGAAGNNNNNNNNNNNNNNNNNNNNNN 634
QY 336 GAGATTGTAGATCTCAGCAAACTCCGAGTGTGAAGTTCGGCCCACTGTGTGACATA 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 633 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 574
QY 336 CACTTTTGCTGCGCAAGCTGTGCAACAATTAACAACGACAGCATGATTCCTGCACAT 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 573 CACCTCTGCGCCGCCACTGCTGGAACAGCACGAGCGAGTGTGATCCCATGCT 514
QY 456 GGGACTTGTATTTGCTACACACATCTCATTTGCCAAAGTTGTTCCAGTTAGACAG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 513 CGCGGAGAGGCTCTGTAGACAGATCACTCTTGCCCAAAATGCTGCCCGCATGTTCCCG 454
QY 516 GATATCACTACCAACAATGAGATATTCTCGAGGTGAGGTTGCTAGACTTGAAC 575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 AATATCCCTACACCAAGTGTAGTACTCCCTAAGTTGCGGCTGCGCTCGGAC 394

```

```

QY 576 ATCTGATCCACCATTAACCAAGTATAGAGTTCCTGAGGTCTTCACCAATCTCAAC 635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 393 ATCCGGGTCCACCATCAACAGAGGTGTAGAAAGTCTCTCATGTAGTNNNNNACCTCGAC 334
QY 636 TCTTGCTGTTTGAACCTGAGAAAGCCTTAGATCCAAAGCATTAAGTACCTCTTTTG 695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 CCTGGGCTGTGACACCATGATGAGCGCTTGAGCTGCAAGCGGTGTGACAGGTCTGCGC 274
QY 696 GCCATPAGTAACTTTAGATGATGATCTATTAAAGCATTAAGACGCTTCACAACAC 755
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 273 CCCGTAGCTGACCTGAGGTGTGCTGCCGAGCAAGGCGTCCAGACGCTCGNNNNNNNN 214
QY 756 TCTGCTACTATAAGAGGCTCT 779
DB 213 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 190

RESULT 8
BE498304/c
LOCUS      BE498304      505 bp      mRNA      linear      EST 04-AUG-2000
DEFINITION WHE0963_B10_C19ZS wheat pre-anthesis spike cDNA library Triticum
ACCESSION  BE498304
VERSION     BE498304
KEYWORDS    BE498304.1  GI:9697017
SOURCE      EST.
             bread wheat.
             Triticum aestivum
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
             ; Triticeae; Triticum.
             1 (bases 1 to 505)
REFERENCE   1 (bases 1 to 505)
AUTHORS     Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
             ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
             Seaton,C.L. and Tong,J.C.
TITLE       The structure and function of the expressed portion of the wheat
             genomes - Pre-anthesis spike cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Olin Anderson
             US Department of Agriculture, Agriculture Research Service, Pacific
             West Area, Western Regional Research Center
             800 Buchanan Street, Albany, CA 94710, USA
             Tel: 5105595773
             Fax: 5105595818
             Email: oanderson@wp.usda.gov
             Sequence have been trimmed to remove vector sequence and low
             quality sequence with phred score less than 20
             Seq primer: Stratagene SK primer.
FEATURES
SOURCE
             1. 505
               /organism="Triticum aestivum"
               /cultivar="Chinese Spring"
               /db_xref="taxon:4565"
               /clone="WHE0963_B10_C19"
               /clone_lib="wheat pre-anthesis spike cDNA library"
               /tissue-type="Spike before anthesis"
               /dev_stage="Adult plant"
               /lab_host="E. coli SOLR"
               /note="vector: Lambda Uni-ZAP XR, excised phagemid;
               Site.1: EcoRI; Site.2: XhoI; Plants were grown in the
               greenhouse. Whole spike with awns trimmed, white, green
               and yellow anther were collected and total RNA, and
               poly(A) RNA were prepared, a cDNA library was made, and
               the cDNA clones were in vivo excised to give plusscript
               phagemids in the TJ Close lab (Choi, Close, Fenton) at
               the University of California, Riverside. Plasmid DNA
               preparations and DNA sequencing were performed in the OD
               Anderson lab (all other authors)."
BASE COUNT  99 a      148 c      160 g      98 t
ORIGIN
Query Match      23.2%; Score 198.4; DB 10; Length 505;
Best Local Similarity 67.3%; Pred. No. 8.4e-25;

```

Matches 280; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 364 GTGTGAAGTTCTGGCCACCTGTGTGATACATCTTTGCTGCCAAGCTGTGGAAC 423
 |||||
 Db 504 GTGTGAAGTTCTGGCCACCTGTGTGATACATCTTTGCTGCCAAGCTGTGGAAG 445

QY 424 AATTAACAGCAGCAGTGAATTCGCAAGTGGAGTGTGATTTGTTGTAACACATC 483
 |||||
 Db 444 AGTACGACGACGAGCGGTGATCCCATGGTCGAGGAGGCTCTGTACACATCACC 385

QY 484 TCATTTGCCAAAGTTGTTCAGTTGTAGCAGAGGATATCAGTACCAACCAATGAGATAT 543
 |||||
 Db 384 TCCGCCCGGACGACGACGATGTATCCGGGATATCTGTACAAAGCAGTGGAGATAC 325

QY 544 TCTCGAGGTGAGGTTGCTAGAGACTTGTGAACATCTGTGATCCACCAATGAGATATG 603
 |||||
 Db 324 TCCCTAAGTTGGATGCTGTGAGTGTGACATCTGTGCTACACAGAGTGTGATC 265

QY 604 AAGTCTGAGGCTTCTCCACCAATCTCAACTCTGTGCTGTGTTGAACCTGAGAGGC 663
 |||||
 Db 264 AAGGCTCTCATCTATGTCGCCGCCACCTCAACCTGGGCTGTGGCGACCATGAGCGC 205

QY 664 CTGATTCACAGCATTAGTACCTCTTGTGGCATAGTAACTTTAGAGTATGAT 723
 |||||
 Db 204 TTGAGCTCGACGCGTGGACAGGCTCTGTCCGAAAGTCAACCTGAGGTTGTGCTC 145

QY 724 CTATTAAAGCATCAAGACGCTCCCAACAACCTGCTTACTATAGAGGCTCTCT 779
 |||||
 Db 144 CGGACGAGGCTGTCACGCTCCGCCCAACCTGCAACCAACGAGGCTCTCT 89

RESULT 9
 BF483056/c 491 bp mRNA linear EST 06-DEC-2000
 LOCUS WHE2314.C03_E06ZS Wheat pre-anthesis spike cDNA library Triticum
 DEFINITION whe2314.C03_E06, mRNA sequence.
 ACCESSION BF483056
 VERSION BF483056.1 GI:11566357
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 491)
 REFERENCE
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Pre-anthesis spike cDNA library
 Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.
 FEATURES
 source
 1.491
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE2314.C03_E06"
 /clone_lib="Wheat pre-anthesis spike cDNA library"
 /tissue_type="Spike before anthesis"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /note="Vector: lambda Uni-ZAP XR, excised phagemid;
 Site_1: EcoRI; Site_2: XhoI; Plants were grown in the

greenhouse. Whole spike with awns trimmed, white, green
 and yellow anther were collected and total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give pBluescript
 phagemids in the T7 close lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 93 a 145 c 151 g 101 t 1 others

ORIGIN

Query Match 23.0%; Score 196.8; DB 12; Length 491;
 Best Local Similarity 67.5%; Pred. No. 1.0e-24;
 Matches 276; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 371 AGTTCTGGCCGACCTGTGTGATACATCTTTGCTGCCAAGCTGTGGAACATATTA 430
 |||||
 Db 491 AGTTCTGGCCGACCTGTGTGATACATCTTTGCTGCCAAGCTGTGGAACATATTA 432

QY 431 ACACGACAGATGAATTCGCACTGTGGACTTGGATTTGTACACACAATCTCATTC 490
 |||||
 Db 431 GCACGAGCGATGATGCCATGCTCGACGAGGCTCTGTACACATCATTCTGCTGCC 372

QY 491 CAAGGTTGTTCCAGTGTAGCAGGATATCAGTACCAACCAATGAGATATTCGGA 550
 |||||
 Db 371 NGAGGATGACACGATGTCACGAGGATCTGTCAACACCAATGAGATATTCCTAA 312

QY 551 GGTGAGGTTGCTAGACTTGAACATCTGGATTCACCAATGAGATATTCGGA 610
 |||||
 Db 311 GGTGAGGATGCTGTGAGATCTGTGAGCATCTGGTCTACACAGTGTATAGAGTCC 252

QY 611 TGAGGTTTCCACCAATCTCAACTCTTGTGTTTGAACCTGAGAGCCTTAGAT 670
 |||||
 Db 251 TCATCTATGTCGCCGCCACCTCAACCTGTGCTGGGACCATGAGCTTGTGAGCT 192

QY 671 CCAAGCCATTAGTACACTCTTGTGGCATAGTAACCTTTAGAGTATGATCTATTA 730
 |||||
 Db 191 CGCAGCCGTTGACACGCTCTGTCCAGAAAGAACTGAGGTTGTGCTCGGATGA 132

QY 731 ACGGATCAGAGCTCTCAACAACCTGCTTACTATAGAGGCTCTCT 779
 |||||
 Db 131 AGGGGTCACACAGCTGCCCAACAACCTGCCAACCACAGCGGTCTCT 83

RESULT 10
 AV937451 542 bp mRNA linear EST 18-JAN-2002
 LOCUS AV937451/c
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone Bah11n08 5', mRNA sequence.
 ACCESSION AV937451
 VERSION AV937451.1 GI:18233248
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. spontaneum.
 ORGANISM Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 542)
 REFERENCE
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 CONTACT: Tadashi Shin-1
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6656
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 FEATURES
 source
 1.542
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"

Db 259 GGGATGCTGACACCATCCAGTCAAGTACTCTTCTAGTATGGTGGTGAATGCGCTTGA 200
 Oy 574 ACATCTGATCCACCATTAACCAAGTATAGAGTCTTGAGTCTTCTCCACCAATCTCA 633
 Db 199 GCGTCTGATCCACCAATATCAGGGTGTGTAGAACTCTCATCTCATCTGACCAAGAACTCA 140
 Oy 634 ACTCTGGCTGTTTGAACCTGACAGAGCCCTTGAATCCAAATTCATTTGACCTCTCTT 693
 Db 139 ACTCTGCTTACTTACTTACATTTGACAGATGCTCTTACTGACACCTGCCAGAACTAGCTCA 80
 Oy 694 TGGCCATTAAGTAACCTTTAGAGTGTATGATCTATTAAACGATCAAGAACTCTCCACA 753
 Db 79 TTGTTGTAGGCTATCCTTAATGGAACGGTTGATGTAATGATCAAGCAATCTTGACANA 20
 Oy 754 AC 755
 Db 19 AC 18

RESULT 14

BJ448552/c

LOCUS BJ448552 671 bp mRNA linear EST 23-MAY-2002
 DEFINITION BJ448552 K. Sato unpublished cDNA library, cv. Akashinriki
 vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
 baak20f16 5', mRNA sequence.

ACCESSION

BJ448552

VERSION

BJ448552.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1. 671
 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Akashinriki"
 /db_xref="taxon:112509"
 /clone="baak20f16"
 /clone_lib="K. Sato unpublished cDNA library, cv.
 Akashinriki vegetative stage leaves"
 /tissue_type="leaves"
 /dev_stage="vegetative stage"
 BASE COUNT 189 a 142 c 166 g 173 t 1 others

Query Match 19.2%; Score 164; DB 13; Length 671;
 Best Local Similarity 60.5%; Pred. No. 6e-19;
 Matches 288; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

Oy 270 AAGTCTTCTCCGCGACGACCTCCCTGACAAATTTGAAAACGCGGCCACGGG 329
 Db 501 AACCTTCTCCGCTGATCCACCTTCCCTTGACA--GTTGAAATATGAGGACGAC 445
 Oy 330 AAGCCGAGATTTAGATCTCAGCAAACTCCGAGTGTGAGTCTGCGCCACCTGG 389
 Db 444 AACGTTTGTGTGCTACTGCGCGTCAAAAGTCTCTGACGCTGAGTCTTGTGCGGACGCTGG 385
 Oy 390 TGCATACACTGTTTGCCTGCCAAGCTGTGCAAAACATATTAACGACGATGAATTC 449
 Db 384 TGCAAAACCTGTACCCCTGCTGCTGCTGCAACAGCAAAATACCATCCTGGTGATACC 325

Oy 450 TCCAGTGGGACTTGGATTTTCTGAACACAAATCTCATTTGCCAAGGTTTCCAGTTGT 509
 Db 324 AGATCTTGGTTTGGTCTTTTCAATACATCAAGCTCTGCGCAAGCTGGACCACTTGT 265
 Oy 510 ACCAGGATATCATGTCACCAACCAATGAGATATTTCTGGAGTGGAGTTTCTAGACT 569
 Db 264 TCCAGGAGATGTGACACCATCCAGTCAAGTACCTCCCTATGATGGTGAATGGGCT 205
 Oy 570 TGGAACTCTGATCCACCATTAACCAAGTATAGAACTTCTGAGTCTTCTCCACCAAT 629
 Db 204 TGGACGCTCTGGATCCACCAATATCAGGGTGTGTAGAACTCTCATGCTACTCCACGNA 145
 Oy 630 CTCACCTCTGGCTGTTTGAACCTGAGAGGCTTGTGATCCAGCAATAGTACCTC 689
 Db 144 ATCACTGCTGCTTACTTACTTACATTCGACATGCTCTTACTGACACCTGCCAGAACTG 85
 Oy 690 TCTTGGCCATTAAGTAACCTTTAGAGTGTATGATCTATTAAACGATCAAGAACT 745
 Db 84 CCTATTGTTGTAGGCTATCCTTAATGGAACGGTTGATGTAATGATCAAGCAAT 29

RESULT 15

BJ315664/c

LOCUS BJ315664 597 bp mRNA linear EST 09-APR-2002
 DEFINITION BJ315664 Y. Ogihara unpublished cDNA library, Wh_yf Triticum
 aestivum cDNA clone whyf19117 5', mRNA sequence.

ACCESSION

BJ315664

VERSION

BJ315664.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1. 597
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whyf19117"
 /clone_lib="Y. Ogihara unpublished cDNA library, Wh_yf"
 /tissue_type="spikelet at early flowering"
 /dev_stage="Feekes' scale 6"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid:
 Site.1: EcoRI; Site.2: XhoI. Plants were grown under
 hydroponic conditions at UC Davis, salt stressed for 12
 hours, and for 7 days, then dissected and frozen (Akhunov
 in J. Dvorak Lab). Total RNA was prepared from shoot
 tissue, equal quantities of RNA were pooled from the two
 samples, polyA was purified from the pooled RNA, a cDNA
 library was made, and the cDNA clones were in vivo
 excised to give plasmid phagemids in the T3 Close Lab
 at the University of California, Riverside (Akhunov, Chin
 , Choi, Close, Fenton, Kianlian, Otto, Simons, Zhang).
 Plasmid DNA preparations and DNA sequencing were
 performed in the OD Anderson lab (all other authors)."

BASE COUNT 153 a 151 c 143 g 147 t 3 others

Query Match 18.4%; Score 157.2; DB 13; Length 597;
 Best Local Similarity 59.0%; Pred. No. 9.4e-18;
 Matches 289; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Db 361 CGAGTGTGAAGTTGGGGCCACCCTGGTGATACACTGTTTGCCTGCCAACCTGTGA 420
Qy 421 AACAAATATAACACGACGATGAATTCCTGCAGTGGAGTTCGATTTTGTAAACACA 480
Db 421 AACAAATATAACACGACGATGAATTCCTGCAGTGGAGTTCGATTTTGTAAACACA 480
Qy 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGCAGGATATCACTACCAACAATGGAGA 540
Db 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGCAGGATATCACTACCAACAATGGAGA 540
Qy 541 TATTCGAGAGTGAGGTTGCTGAGCACTTGGAACATTCGATTCACCAATACCAAGTA 600
Db 541 TATTCGAGAGTGAGGTTGCTGAGCACTTGGAACATTCGATTCACCAATACCAAGTA 600
Qy 601 TAGAATTCCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTTGAACCTGAGA 660
Db 601 TAGAATTCCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTTGAACCTGAGA 660
Qy 661 GGCCTTAGATCCAGCCATTTAGTACCTCTCTTGGCCATTAAGTAACCTTTAGAGTGA 720
Db 661 GGCCTTAGATCCAGCCATTTAGTACCTCTCTTGGCCATTAAGTAACCTTTAGAGTGA 720
Qy 721 GATCTATTAAAGGATCAAGAACTGCTCCACAACTGCTTACTATAAGAGGCTCTT 780
Db 721 GATCTATTAAAGGATCAAGAACTGCTCCACAACTGCTTACTATAAGAGGCTCTT 780
Qy 781 ATATTATAGACATCTTTGATCTTGAACAACCTCGTGATTCCTGAGCCGGGG 840
Db 781 ATATTATAGACATCTTTGATCTTGAACAACCTCGTGATTCCTGAGCCGGGG 840
Qy 841 ATCCACTAGTTCTAGA 856
Db 841 ATCCACTAGTTCTAGA 856

RESULT 2
US-09-060-726A-1/C
; Sequence 1, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS.026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(590)
US-09-060-726A-1

Query Match 98.4%; Score 842.4; DB 4; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-213;
Matches 854; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CTCGAGTTTTTTTTTTTTTTTTTATAAATAAACACTTCATTTTCATGATTAATA 60
Db 855 CTCGAGTTTTTTTTTTTTTTTTTATAAATAAACACTTCATTTTCATGATTAATA 796
Qy 61 TAATTATCGATCAGACATATATATAGTAAACACTCTCATTTTCTCCCTCTCATTT 120
Db 795 TAATTATCGATCAGACATATATATAGTAAACACTCTCATTTTCTCCCTCTCATTT 736
Qy 121 TTAATTACACACTATATATTTGAACCTATAGGATCATCAGCGTCTGTTACTCGATCA 180
Db 735 TTAATTACACACTATATATTTGAACCTATAGGATCATCAGCGTCTGTTACTCGATCA 676

Qy 181 TAAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 675 TAAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 616
Qy 241 CAATTGCTTATTAAGGAAGACCATCTTAAGTCTTCTTCTCCGACCATCTCTCC 300
Db 615 C-ATTGCTTATTAAGGAAGACCATCTTAAGTCTTCTTCTCCGACCATCTCTCC 557
Qy 301 TGACAAATTTAGAAAAGTGGGCGGACGGGAGGCGGAGGATTTAGATTTCTCAGAACTCG 360
Db 556 TGACAAATTTAGAAAAGTGGGCGGACGGGAGGCGGAGGATTTAGATTTCTCAGAACTCG 497
Qy 361 CGAGTGTGAAGTTTGGGGCCACCCTGGTGATACACTGTTTGCCTGCCAACCTGTGA 420
Db 496 CGAGTGTGAAGTTTGGGGCCACCCTGGTGATACACTGTTTGCCTGCCAACCTGTGA 437
Qy 421 AACAAATATAACACGACGATGAATTCCTGCAGTGGAGTTCGATTTTGTAAACACA 480
Db 436 AACAAATATAACACGACGATGAATTCCTGCAGTGGAGTTCGATTTTGTAAACACA 377
Qy 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGCAGGATATCACTACCAACAATGGAGA 540
Db 376 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGCAGGATATCACTACCAACAATGGAGA 317
Qy 541 TATTCGAGAGTGAGGTTGCTGAGCACTTGGAACATTCGATTCACCAATACCAAGTA 600
Db 316 TATTCGAGAGTGAGGTTGCTGAGCACTTGGAACATTCGATTCACCAATACCAAGTA 257
Qy 601 TAGAATTCCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTTGAACCTGAGA 660
Db 256 TAGAATTCCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTTGAACCTGAGA 197
Qy 661 GGCCTTAGATCCAGCCATTTAGTACCTCTCTTGGCCATTAAGTAACCTTTAGAGTGA 720
Db 196 GGCCTTAGATCCAGCCATTTAGTACCTCTCTTGGCCATTAAGTAACCTTTAGAGTGA 137
Qy 721 GATCTATTAAAGGATCAAGAACTGCTCCACAACTGCTTACTATAAGAGGCTCTT 780
Db 136 GATCTATTAAAGGATCAAGAACTGCTCCACAACTGCTTACTATAAGAGGCTCTT 77
Qy 781 ATATTATAGACATCTTTGATCTTGAACAACCTCGTGATTCCTGAGCCGGGG 840
Db 76 ATATTATAGACATCTTTGATCTTGAACAACCTCGTGATTCCTGAGCCGGGG 17
Qy 841 ATCCACTAGTTCTAGA 856
Db 16 ATCCACTAGTTCTAGA 1

RESULT 3
US-07-644-372-1/C
; Sequence 1, Application US/07644372
; Patent No. 5416009
; GENERAL INFORMATION:
; APPLICANT: Lazzeri, Mario E.
; APPLICANT: Nutman, Thomas B.
; APPLICANT: Weis, Niklaus
; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
; TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/644,372
; FILING DATE: 19910123
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-0944
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..507
;
; US-07-644-372-1
;
Query Match      8.4%; Score 71.8; DB 1; Length 822;
Best Local Similarity 51.3%; Pred. No. 5.8e-10;
Matches .217; Conservative 0; Mismatches 202; Indels 4; Gaps 2;

QY 294 CTCCTCTGACAACTTGTAGAAAACGCGCCAGGAGGCGGAGATTGTGATCTCAGC 353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 637 CTCATGTTAGCCTGGAAGAGATTCCGCGCACTGATTTCCAGATGATGTTGTTGC 578
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 354 AACTCGCGAGTGTGAAGTCTGGCG---CCACCTGGTGCAATACACTTTGGCTGCC 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 AAATCATTAATCTTAAATTTGCGGAGTTCCGCATGTGATCCGTGATCTTCC 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 411 AAGCTGTGAAAATATATAACAGACAGCATGATTCCTCGATGGAGATTGATTC 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 517 AGGTGTTTATTAACCAAGATATACAGATTAAGTCTGCTTTCCTGACCTGA 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 471 GTAACACAAATCTAGTCCCAAGGTTG-TTCAGTGTGACGAGGATATCAGTACCA 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 TCCAAATATACATACACTGTCCACTGCTACATTTTGTCCAGAAATTTATATCA 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 530 ACCAATGGAGATTTCTCGAGAGTGAAGGTTGCTAGACTTGAACATCTGGATCCCA 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 ACCAATGGAGCTCTCTGAAATACGGGGTTTTTTCAGATGCTGCGGATCAGTCA 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 TAACCAAGATATGAGTCTGAGGCTCTTCACCAATCTGACCTTGGCTGTTT 649
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 337 TAACGAGCTATATTAAGCTCCAGGTTCCGCAATCCATGATTTGTGCGCTGATCT 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 650 GAACCTGAGAGGCTTATGATCCAGCATTTAGTCACTCTCTTTGGCCATAGTACT 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 277 TTACTGCGCTGCGGCTAAGTATTAATGCCAGATTCAOCCGTGAGATTATGTAATA 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 710 TTA 712
    |||
DB 217 TGA 215
    |||

RESULT 4
US-08-467-948A-3
; Sequence 3, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
```

```

;
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 884..2062
;
; US-08-467-948A-3
;
Query Match      5.5%; Score 47; DB 2; Length 2185;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 802 CTGGAACAAACCTGCTGATTCCTGACAGCCGGGGGATCCAGTATGTTCTAGA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2018 CTCAAACCAACCTGCTGCAATTCCTGCAAGCCGGGGGATCCAGTATGTTCTAGA 2072
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-08-467-947A-3
; Sequence 3, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR1
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,947A
```

```

US-08-482-130C-60/C
; Sequence 60, Application US/08482130C
; Patent No. 5962257
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary L.
; TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, AND USES THEREOF
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,130C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-25-C1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..234
; US-08-482-130C-60
;
Query Match 5.5%; Score 46.8; DB 2; Length 234;
Best Local Similarity 73.2%; Pred. NO. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

QY	835	CGGGGATCCACTGCTCTGA	856
Dd	69	CGGGGATCCACTGCTCTGA	48

RESULT 8

[illegible]

```

Patent No. 6077687
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-906-769-60
Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 775 TCTCTATTATTATAGACATCTTGATCTTGACACAACCTGCTGTAATTCGACGCC 834
      ||||| || ||||| | ||| || ||||| ||||| |||||
DB 129 TATCTGTGAAGATGAGAGCGCGTCATCAACCAACGCTGTCGGAATTCGACGCC 70
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 835 CGGGGATCCACTAGTTCTAGA 856
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 CGGGGATCCACTAGTTCTAGA 48
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 10
US-08-906-616-60/c
Sequence 60. Application US/08906616
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary

```

APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-906-616-60

Query Match
Best Local Similarity 73.2%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCTCTATATTATGACATCTTGATCTTGACAAACCTGCGTGAATTCCTGCACCC 834
DB 129 TATCTGTGATGAGTGAAGCGCGCTCATCCAAACGCTGCGGATTCCTGCACCC 70
QY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 11
US-08-817-795-60/C
Sequence 60, Application US/08817795
Patent No. 6139840
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Yamaka, Miles Yamanaka
APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-817-795-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCTCTATATTATGACATCTTGATCTTGACAAACCTGCGTGAATTCCTGCACCC 834
DB 129 TATCTGTGATGAGTGAAGCGCGCTCATCCAAACGCTGCGGATTCCTGCACCC 70
QY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 12
US-08-485-443B-60/C
Sequence 60, Application US/08485443B
Patent No. 6146870
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/485.443B
APPLICATION NUMBER: US/08/485.443B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
TELEFAX: 303 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-443B-60

Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCCTTATATTTATAGACATCTTGTGTAACAACCTCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTGAATGAGACCGGCTCAATCCAAACGCTCGTGGCAATTCCTGCAGCC 70
OY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 13
US-08-639-075A-60/C
Sequence 60, Application US/08639075A
Patent No. 6150125
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639.075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCCTTATATTTATAGACATCTTGTGTAACAACCTCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTGAATGAGACCGGCTCAATCCAAACGCTCGTGGCAATTCCTGCAGCC 70
OY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 14
US-09-012-431-60/C
Sequence 60, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012.431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 1..234
?      SEQUENCE DESCRIPTION: SEQ. ID NO: 60:
US-09-012-431-60

Query Match          5.5%; Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches    60; Conservative   0; Mismatches   22; Indels     0; Gaps     0;

OY      775 TCTCTTAATATTATAGACATCTTTGATCTTGACAACAACCTCGTGTGAATTCCTGCAGCC 834
         |||||  |||| | ||| || |||||| |||||||||
Db       129 TATCTTGTAAAGATGAGAGCGCCTCAATCCAACCAACGGCTCGGCGAATTCCTGCAGCC 70

OY      835 CGGGGGATCCACTAGTCTAGA 836
         |||||||||||||||||
Db        69 CGGGGGATCCACTAGTCTAGA 48

```

```

RESULT 15
US-09-012-692-60/c
: Sequence 60, Application US/09012692
: Patent No. 6214579
: GENERAL INFORMATION:
: APPLICANT: Grieve, Robert B.
: APPLICANT: Rushlow, Keith E.
: APPLICANT: Wu Hunter, Shirley
: APPLICANT: Frank, Glenn R.
: APPLICANT: Stiegler, Gary
: APPLICANT: Gaines, Patrick J.
: APPLICANT: Silver, Gary
: TITLE OF INVENTION: RNA PROTEASE PROTEINS, NUCLEIC ACID
: TITLE OF INVENTION: MOLECULES AND USES THEREOF
: NUMBER OF SEQUENCES: 190
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sheridan Ross & McIntosh
: STREET: 1700 Lincoln Street, Suite 3500
: CITY: Denver
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80203
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/012.692
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/639,075
: FILING DATE: 24-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Connell, Gary J.
: REGISTRATION NUMBER: 32,020
: REFERENCE/DOCKET NUMBER: 2618-25-C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 863-9700
: TELEFAX: (303) 863-0223
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 234 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..234
: US-09-012-692-60

```

	Query Match	5.5%	Score 46.8;	DB 4;	Length 234;	
	Best Local Similarity	73.2%;	Pred. No. 0.0015;			
	Matches	60;	Conservative	0;	Mismatches 22;	Indels 0; Gaps 0.
Oy	775 TCTCTATATTATAGACACTTTGATCTTGAAACAACCCTCGTGGTAGATTCCTGCAGCC					834
Dd	129 TATCTTTGTGAAGTGGAGACGCCCTCAATCCATCAACCAAACGCTCCTGCCAATTCTTGACCC					70
Oy	835 CCGGGGATCCACTACTTCTAGA					856
Dd	69 CGGGGATCCACTACTTCTAGA					48

Search completed: May 1, 2003, 21:56:17
Job time : 64 secs

Oy	835	CGGGGATCCACTAGTCTAGA	856
Db	69	CGGGGATCCACTAGTCTAGA	48

Query Match	Similarity	Score	DB	Length
1	100.0%	856	10	856
2	100.0%	9e-206		
3	Conservative	0	Mismatches	0
4	Indels	0	Gaps	0
5	1	CTCGAGTTT	TTTTTTTTTTTTTTTTTTTTTTTTTAAATAATTAACACTTCATTTCAATAGATATA	60
6	1	CTCGAGTTT	TTTTTTTTTTTTTTTTTTTTTTTTTAAATAATTAACACTTCATTTCAATAGATATA	60
7	61	TAAATATGCGATC	CACACACTATATTAAGTAAACACTTCATTTCCCTCCCTCCATTT	120
8	61	TAAATATGCGATC	CACACACTATATTAAGTAAACACTTCATTTCCCTCCCTCCATTT	120
9	121	TTATATACACTAT	ATATTTGACACTATATAGCATATCAACCGTGTCTACTGATCA	180
10	121	TTATATACACTAT	ATATTTGACACTATATAGCATATCAACCGTGTCTACTGATCA	180
11	181	TAAATATGCTTAT	TAAATTAATAATTAATAGATGCAATTAATCTCATACAGATAGCAATAT	240
12	181	TAAATATGCTTAT	TAAATTAATAATTAATAGATGCAATTAATCTCATACAGATAGCAATAT	240
13	241	CAATTGGTTATTA	AAAGAAAGCAATCAAAAGTCTTCTCCGACACACTCTCCCTC	300
14	241	CAATTGGTTATTA	AAAGAAAGCAATCAAAAGTCTTCTCCGACACACTCTCCCTC	300
15	301	TGACAAATTTGT	AAACACGCGCCGACGGGAAGCCGAGATATGTATGATCTGACAAACGCG	360
16	301	TGACAAATTTGT	AAACACGCGCCGACGGGAAGCCGAGATATGTATGATCTGACAAACGCG	360
17	361	CGAGTGTTGA	GTCTGCGCCACCTTGCTCATACATGCTGTTCCCTCCCAAGCTGTCGA	420
18	361	CGAGTGTTGA	GTCTGCGCCACCTTGCTCATACATGCTGTTCCCTCCCAAGCTGTCGA	420
19	421	AACAAATATTA	AAACAGACGATGAATTCCTCGAGTGGAGCTTGATTTTCTGTAACACACA	480
20	421	AACAAATATTA	AAACAGACGATGAATTCCTCGAGTGGAGCTTGATTTTCTGTAACACACA	480
21	481	ATCCTATTTGCC	AAAGGTTGTTCCAGTTGTACAGAGGATATAGTCACCAACCAATGGAGA	540
22	481	ATCCTATTTGCC	AAAGGTTGTTCCAGTTGTACAGAGGATATAGTCACCAACCAATGGAGA	540
23	541	TATTCCTCGAG	GTTGAGGTTGCTAGGACTTGGAAATCTGGATCCACCATTAACCAAGTA	600
24	541	TATTCCTCGAG	GTTGAGGTTGCTAGGACTTGGAAATCTGGATCCACCATTAACCAAGTA	600
25	601	TAGAAATTTCC	CGAGGTTCTTCCACCAATCTCACTCTGGCTTTTGAACCTGAGAA	660
26	601	TAGAAATTTCC	CGAGGTTCTTCCACCAATCTCACTCTGGCTTTTGAACCTGAGAA	660
27	661	GCCCTTAATAT	CAAGCCATTAGTCAACCTCTTTGGCCATTAAGTAACTTAAAGTATTT	720
28	661	GCCCTTAATAT	CAAGCCATTAGTCAACCTCTTTGGCCATTAAGTAACTTAAAGTATTT	720
29	721	GATCTATTAA	AGGATCAAGACTTGTAGTCAACCAACTCTGCTTACTATTAAGGGGTCTCTT	780
30	721	GATCTATTAA	AGGATCAAGACTTGTAGTCAACCAACTCTGCTTACTATTAAGGGGTCTCTT	780
31	781	ATATTATTA	AGACATCTTGTGATCTTGAACAAACCTGAGTAAATCTTGAAGGGGGGG	840
32	781	ATATTATTA	AGACATCTTGTGATCTTGAACAAACCTGAGTAAATCTTGAAGGGGGGG	840
33	841	ATCCACTAGT	CTCTAGA	856
34	841	ATCCACTAGT	CTCTAGA	856

APPLICANT: KARDALISKY, Igor
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS.026DVI
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-845-849-1

Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAATACCTTCATTCATGATTAATA 60
DB CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAATACCTTCATTCATGATTAATA 797
61 TAATATCGCATCACACATATATAGTAATAACATCTCATTTTCCCTCCCTCATTT 120
DB TAATATCGCATCACACATATATAGTAATAACATCTCATTTTCCCTCCCTCATTT 737
121 TTATTAACACTTATATATGAACTACTATAGCATATCAGCGTTGCTACTGATCA 180
DB TTATTAACACTTATATATGAACTACTATAGCATATCAGCGTTGCTACTGATCA 677
181 TAAATGCTATTAATTAATTAATACATATGATGATTAATCTATGATGATTAAT 240
DB TAAATGCTATTAATTAATTAATACATATGATGATTAATCTATGATGATTAAT 617
241 CAATTGGTTTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB CAATTGGTTTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 557
301 TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 497
556 TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 497
361 CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
496 CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
421 AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 480
DB AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 377
436 AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 377
481 ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 540
DB ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 317
376 ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 317
541 TATTTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGG 600
DB TATTTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGG 257
316 TATTTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGG 257
601 TAGAAGTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAG 660
DB TAGAAGTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAG 197
256 TAGAAGTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAG 197
661 GGCCTTAGATCAAGCCATTAGTCACTCTTTGGCCATTAAGTAACTTTAGAGTAT 720
DB GGCCTTAGATCAAGCCATTAGTCACTCTTTGGCCATTAAGTAACTTTAGAGTAT 137
196 GGCCTTAGATCAAGCCATTAGTCACTCTTTGGCCATTAAGTAACTTTAGAGTAT 137
721 GATCTTTAAGGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 780
DB GATCTTTAAGGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 77
136 GATCTTTAAGGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 77
781 ATATTTAAGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 840

|||||
DB ATATTTAAGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 17
76 ATATTTAAGAGTGAAGAGTCTCCCAAGAGTCTGTTACTATTAAGAGGTTCTT 17
841 ATCCACTAGTTCTAGA 856
|||||
DB ATCCACTAGTTCTAGA 1

RESULT 4

US-09-845-849-3
Sequence 3, Application US/09845849
Patent No. US2002002935A1
GENERAL INFORMATION:
APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
APPLICANT: WEIGEL, Detlef
APPLICANT: KARDALISKY, Igor
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS.026DVI
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-845-849-3

Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAATACCTTCATTCATGATTAATA 60
DB 1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAATACCTTCATTCATGATTAATA 60
61 TAATATCGCATCACACATATATAGTAATAACATCTCATTTTCCCTCCCTCATTT 120
DB TAATATCGCATCACACATATATAGTAATAACATCTCATTTTCCCTCCCTCATTT 120
121 TTATTAACACTTATATATGAACTACTATAGCATATCAGCGTTGCTACTGATCA 180
DB TTATTAACACTTATATATGAACTACTATAGCATATCAGCGTTGCTACTGATCA 180
121 TTATTAACACTTATATATGAACTACTATAGCATATCAGCGTTGCTACTGATCA 180
181 TAAATGCTATTAATTAATTAATACATATGATGATTAATCTATGATGATTAAT 240
DB TAAATGCTATTAATTAATTAATACATATGATGATTAATCTATGATGATTAAT 240
181 TAAATGCTATTAATTAATTAATACATATGATGATTAATCTATGATGATTAAT 240
241 CAATTGGTTTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB CAATTGGTTTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
241 CAATTGGTTTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
301 TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
301 TGACAAATTTAGAAAACCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
361 CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
361 CGAGTGTGAGAGTTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
421 AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 480
DB AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 480
421 AACAAATTAACAGACAGATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGG 480
481 ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 540
DB ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 540
481 ATTCATTTGCGCAAGGTTGTTCCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAG 540
541 TATTTCTCGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAG 600
|||||

Db	541	TATTCGGAGGTAGGGTCTCTAGGACTTGGAACTATCGGATCCACCATTAACCAANGTA	6000
Qy	601	TAGAAGTCCCGAGAGCTCTTCCACCAATCTCAACTCTTGCTGTGTTGAACCTAGAA	6666
Db	601	TAGAAGTCCCGAGAGCTCTTCCACCAATCTCAACTCTTGCTGTGTTGAACCTAGAA	6666
Qy	661	GGCCTTAGATCAAGCCATTAGTACCCCTCTTTGGCCATTAAGTAACCTTAGAGTATT	7200
Db	661	GGCCTTAGATCAAGCCATTAGTACCCCTCTTTGGCCATTAAGTAACCTTAGAGTATT	7200
Qy	721	GATCATTAAGCGGATGAAAGAGCTGCCAACACTCTGCTACTATAAGAGGTCTT	7800
Db	721	GATCATTAAGCGGATGAAAGAGCTGCCAACACTCTGCTACTATAAGAGGTCTT	7800
Qy	781	ATATTTATAGACATCTTTGATCTTGAACAACACCTGCTGTAATTCCTGCAGCCCGGGG	8400
Db	781	ATATTTATAGACATCTTTGATCTTGAACAACACCTGCTGTAATTCCTGCAGCCCGGGG	8400
Qy	841	ATCCACTAGTCTAGA 856	
Db	841	ATCCACTAGTCTAGA 856	

```

RESULT 5
US-09-938-842A-2635/C
Sequence 2635, Application US/09938642A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2635
LENGTH: 528
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2635

```

Query Match	44.1%	Score 377.6	DB 9	Length 528
Best Local Similarity	82.2%	Pred. No. 2.1e-85		
Matches 434	Conservative	0	Mismatches 94	Indels 0
			Gaps 0	
QY 267	CTAAAGTCTTCTTCCTCCGACACCTCTCCCTCGACAAATGTAGAAACTCGGCGCC	326		
Db 528	CTACGTTTCTTCTTCCCCACACCACTTCTCCCTCTGGCAGTTGAAGTAGAGGCAACCC	469		
QY 327	GGGAAGGCCGAGATTGTAGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGCGCACCC	386		
Db 468	AGGAAGACCAGAATGTAGATCTCAGCAAACTCAGAGAGTTGAACTGTGGCGCCACCC	409		
QY 387	TGTGTCAATACACTGTTTGGCTTCGCACAACTGTTCGAAAACATATTAACACGACAGTAGAT	446		
Db 408	CGGTGCAATAAACCGTTTCTTCCGAGTGTCCGGAAACATACCAACACATATTCAGTAGAT	349		
QY 447	TTCCTGCAGTGGGACCTTGGATTTTGGTAAACACACAATCTCATTTGCCAAAGTTGTTCCAGT	506		
Db 348	TCCCGAGGGGGAGACTGGACTCTCGTACACACCACTCATATGCCCCAAAGGCAATTCCAGT	289		
QY 507	TGTAGCAGGAGATATCAGTACACCAACCAATGGAGATATCTCGGAGTGAAGGTTTCTGAG	566		
Db 288	GGTGGCAGGATATTCAGTACCAACCACTGGAGATATCTCGTGGTGAAGGTTTCTTGG	229		

[illegible]

```

RESULT 6
US-09-938-842A-1501/c
: Sequence 1501, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227, 866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264, 647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300, 111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1501
: LENGTH: 534
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1501

```

Query Match	Best Local Similarity	Score	DB	Length
20.7%	60.6%	176.8	9	534
Matches	Conservative	0	Mismatches	197
			Indels	3
			Gaps	1

Db 145 AAAACCCCTAAATAAATAACTGCTGCCGAATTCCTGCAGCCGGGGATCCAC 86
 QY 847 TACTCTAGA 856
 |||||
 Db 85 TACTCTAGA 76

RESULT 10
 US-10-074-095-248
 ; Sequence 248, Application US/10074095
 ; Publication No. US2003007704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC008C1
 ; CURRENT APPLICATION NUMBER: US/10/074,095
 ; PRIOR FILING DATE: 2002-02-14
 ; PRIOR APPLICATION NUMBER: 09/764,860
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,447
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/218,290
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/225,757
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,267
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/216,880
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/251,869
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/235,834
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/234,274
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/234,223
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/228,924
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/224,518
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,369
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/224,519
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,964
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/241,809
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/249,299
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/236,327
 ; PRIOR FILING DATE: 2000-09-29

;; PRIOR APPLICATION NUMBER: 60/241,785
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/244,617
 ;; PRIOR FILING DATE: 2000-11-01
 ;; PRIOR APPLICATION NUMBER: 60/225,268
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/236,368
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/251,856
 ;; PRIOR FILING DATE: 2000-12-08
 ;; PRIOR APPLICATION NUMBER: 60/251,868
 ;; PRIOR FILING DATE: 2000-12-08
 ;; PRIOR APPLICATION NUMBER: 60/229,344
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/234,997
 ;; PRIOR FILING DATE: 2000-09-25
 ;; PRIOR APPLICATION NUMBER: 60/229,343
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,345
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,287
 ;; PRIOR FILING DATE: 2000-09-01
 ;; PRIOR APPLICATION NUMBER: 60/229,513
 ;; PRIOR FILING DATE: 2000-09-05
 ;; PRIOR APPLICATION NUMBER: 60/231,413
 ;; PRIOR FILING DATE: 2000-09-08
 ;; PRIOR APPLICATION NUMBER: 60/229,509
 ;; PRIOR FILING DATE: 2000-09-05
 ;; PRIOR APPLICATION NUMBER: 60/236,367
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/237,039
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,038
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/236,370
 ;; PRIOR FILING DATE: 2000-09-29
 ;; PRIOR APPLICATION NUMBER: 60/236,802
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,037
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/237,040
 ;; PRIOR FILING DATE: 2000-10-02
 ;; PRIOR APPLICATION NUMBER: 60/240,960
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/239,935
 ;; PRIOR FILING DATE: 2000-10-13
 ;; PRIOR APPLICATION NUMBER: 60/239,937
 ;; PRIOR FILING DATE: 2000-10-13
 ;; PRIOR APPLICATION NUMBER: 60/241,787
 ;; PRIOR FILING DATE: 2000-10-20
 ;; PRIOR APPLICATION NUMBER: 60/246,474
 ;; PRIOR FILING DATE: 2000-11-08
 ;; PRIOR APPLICATION NUMBER: 60/246,532
 ;; PRIOR FILING DATE: 2000-11-08
 ;; PRIOR APPLICATION NUMBER: 60/249,216
 ;; PRIOR FILING DATE: 2000-11-17
 ;; PRIOR APPLICATION NUMBER: 60/249,210
 ;; PRIOR FILING DATE: 2000-11-17
 ;; PRIOR APPLICATION NUMBER: 60/226,681
 ;; PRIOR FILING DATE: 2000-08-22
 ;; PRIOR APPLICATION NUMBER: 60/225,759
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/225,213
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/227,182
 ;; PRIOR FILING DATE: 2000-08-22
 ;; PRIOR APPLICATION NUMBER: 60/225,214
 ;; PRIOR FILING DATE: 2000-08-14
 ;; PRIOR APPLICATION NUMBER: 60/235,836
 ;; PRIOR FILING DATE: 2000-09-27
 ;; PRIOR APPLICATION NUMBER: 60/230,438
 ;; PRIOR FILING DATE: 2000-09-06
 ;; PRIOR APPLICATION NUMBER: 60/215,135

```

: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 60/225,266
: PRIOR FILING DATE: 2000-08-14
: PRIOR APPLICATION NUMBER: 60/249,218
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,208
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,213
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,212
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,207
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,245
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,244
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,217
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,211
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,215
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,264
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,214
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,297
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/232,400
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/231,242
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,081
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,080
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,414
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,244
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/233,064
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/233,063
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,397
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,399
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,401
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/241,808
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,826
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,786
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,221
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/246,475
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: 60/231,243
: PRIOR FILING DATE: 2000-09-08

```

Query Match 5.6%; Score 48.2; DB 9; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

OY 780 TATATTATAGACATCTTGATCTTGACAAACCTCGTCGATTCCTGAGCCGGGG 839
DB 229 TGTGTTCTATAAAGATATTGCTGTGTAGTTTCTCGTGGCAATTCCTGAGCCGGGG 288
OY 840 GATCCACTAGTTCTAGA 856

```

```

Db 289 GATCCACTAGTTCTAGA 305

```

```

RESULT 11
US-09-764-860-248
: Sequence 248, Application US/09764860
: Patent No. US20020094953A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC008
: CURRENT APPLICATION NUMBER: US/09/764,860
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1198
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 248
: LENGTH: 367
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (345)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-248

```

Query Match 5.6%; Score 48.2; DB 10; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

OY 780 TATATTATAGACATCTTGATCTTGACAAACCTCGTCGATTCCTGAGCCGGGG 839
DB 229 TGTGTTCTATAAAGATATTGCTGTGTAGTTTCTCGTGGCAATTCCTGAGCCGGGG 288
OY 840 GATCCACTAGTTCTAGA 856
DB 289 GATCCACTAGTTCTAGA 305

```

```

RESULT 12
US-09-925-300-816/c
: Sequence 816, Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben,
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05988
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 816
: LENGTH: 551
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (2)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (15)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-816

```

Query Match 5.6%; Score 48; DB 10; Length 551;
Best Local Similarity 75.0%; Pred. No. 0.022;
Matches 60; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Query Match	5.6%;	Score 47.6;	DB 10;	Length 560;
Best Local Similarity	75.6%;	Pred. No. 0.028;		
Matches	59;	Conservative	0;	Mismatches 19;
			Indels	0;
			Gaps	0;

Search completed: May 1, 2003, 23:35:13
Job time : .159.5 secs

Search completed: May 1, 2003, 23:35:13
Job time : .159.5 secs